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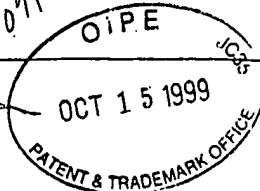


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print 09/025,769.



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- Ans C*
T2160
D
- (i) APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
 - (ii) TITLE OF INVENTION: Protein/(Poly)peptide libraries
 - (iii) NUMBER OF SEQUENCES: 373
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: James F. Haley, Jr., Esq. c/o FISH & NEAVE
 - (B) STREET: 1251 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: United States of America
 - (F) ZIP: 10020
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 - (vi) CURRENT APPLICATION DATA
 - (A) APPLICATION NUMBER: 09/025,769
 - (B) FILING DATE: 18-FEB-1998
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: EP 95 11 3021.0
 - (B) FILING DATE: 18-AUG-1995
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: James F. Haley, Jr., Esq.
 - (B) REGISTRATION NUMBER: 27,794
 - (C) REFERENCE/DOCKET NUMBER: MORPHO/5
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212)596-9000
 - (B) TELEFAX: (212)596-9090

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Ala Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15
Gly Gly Gly Ser
20

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCAGCGGGTG GCGGTTCTGG CGGCGGTGGG AGCGGTGGCG GTGGTTCTGG CGGTGGTGGT
60

TCCGATATCG GTCCACGTAC GG
82

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AATTCGGTAC GTGGACCGAT ATCGGAACCA CCACCGCCAG AACACCGCC ACCGCTCCCA 60

CCGCCGCCAG AACCGCCACC CGC

83

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 28..45
- (D) OTHER INFORMATION: /product= "6 random codons by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATACGGCCG TGTATTATTG CGCGCGTNNK NNNNNNNNNK NNNNGGATTA TTGGGGCCAA 60
GGCACCCCTG 69

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 28..57
- (D) OTHER INFORMATION: /product= "10 random codons by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 58..60
- (D) OTHER INFORMATION: /product= "random codon by trinucleotide mutagenesis (TTT/ATG)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

- (B) LOCATION:64..66
(D) OTHER INFORMATION:/product= "random codon by
trinucleotide mutagenesis (GTT/TAT)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GATACGGCCG TGTATTATTG CGCGCGTNNK NNKNNKNNKN NKNNKNNKNN KNNKNNKWK 60
GATKWTGGG GCCAAGGCAC CCTG 84

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATACGGCCG TGTATTATTG C
21

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGGTGCCT TGGCCCC

17

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCAGAAGGCG AACGTCC
17

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:39..41
(D) OTHER INFORMATION:/product= "random codon (mixture of GCT, CGT, CAT, TCT, TAT)"

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:42..53
(D) OTHER INFORMATION:/product= "random codons by trinucleotide mutagenesis (19 aa, no Cys)"

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:57..59
(D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19 aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGGAAGCTGA AGACGTGGGC GTGTATTATT GCCAGCAGBV TNNKNNKNNK NKKCCGNNKT 60
TTGGCCAGGG TACGAAAGTT 80

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AAC TTCGTA CCCTGGCC

18

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 21..23

(D) OTHER INFORMATION: /product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 27..35

(D) OTHER INFORMATION: /product= "random codons by trinucleotide mutagenesis (19 aa, no Cys)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 36..41

(D) OTHER INFORMATION: /product= "random codons by mixed monomers (A/G A/C/G T)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 42..44

(D) OTHER INFORMATION: /product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 48..50

(D) OTHER INFORMATION: /product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

AGGGTCTCGA GTGGGTGAGC NNKATTNNKN NKNNKRVTRV TNNKACCNNK TATGCGGATA 60
GCGTGAAAGG CCGTTTTACC ATTTACGTG ATAATTCGAA AAACACCA 108

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:21..23
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:27..32
- (D) OTHER INFORMATION:/product= "random codons by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:33..38
- (D) OTHER INFORMATION:/product= "random codons by mixed monomers (A/G A/C/G T)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:39..41
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:45..47
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGGGTCTCGA GTGGGTGAGC NNKATTNNKN NKRVTTRVTTNN KACCNNKTAT GCGGATAGCG 60
TGAAAGGCCG TTTTACCATT TCACGTGATA ATTCGAAAAA CACCA 105

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGGTGT TTTT CGAATTATCA

20

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Asp	Ile	Val	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Pro	Gly
1				5					10					15	
Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser
			20					25					30		
Asn	Gly	Tyr	Asn	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser
		35					40					45			
Pro	Gln	Leu	Leu	Ile	Tyr	Leu	Gly	Ser	Asn	Arg	Ala	Ser	Gly	Val	Pro
	50					55					60				
Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile
65				70					75					80	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Ala
			85					90						95	
Leu	Gln	Thr	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys
			100					105					110		
Arg															

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	

224

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Asn Ser Pro
85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg.

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln
1				5				10						15	
Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn	Ile	Gly	Asn	Asn
		20					25						30		
Tyr	Val	Ser	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu
		35					40					45			
Ile	Tyr	Asp	Asn	Asn	Lys	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser
	50				55					60					
Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln
65				70					75					80	
Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Thr	Trp	Asp	Asp	Ser	Leu
			85					90						95	
Ser	Gly	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln
		100					105						110		

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser
 85 90 95
 Ser Thr Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr
 1 5 10 15
 Ala Arg Ile Thr Cys Ser Gly Asp Ser Leu Gly Ser Lys Tyr Ala Ser
 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Asp
 35 40 45
 Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn
 50 55 60
 Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val Gln Ala Glu Asp
 65 70 75 80
 Glu Ala Asp Tyr Tyr Cys Gln Ser Trp Asp Ser Ser Gly Asn Val Val
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ala Pro Gly Tyr Cys Ser Gly Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Asn Pro Asn Ser Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Gly Asp Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110
Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Glx Val Thr Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala His Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Gly Arg Gly Gly Gly Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Gly Gly Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30
 Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
 35 40 45
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60
 Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Asp Pro Gly Gly Phe Asp Val Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser

115

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln His
 85 90 95
 Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110
 Arg Thr

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
 85 90 95
 Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr

100

105

110

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1           5           10           15
Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20           25           30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35           40           45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50           55           60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85           90           95
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100          105          110
Lys Arg Thr
115

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(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30
 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
 85 90 95
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr
 85 90 95
 Pro Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly

100

105

110

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15
 Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60
 Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Val
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln

100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60
 Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Gln
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Ala	Ile	Ser	Gly	Asp	Ser	Val	Ser	Ser	Asn
			20					25					30		
Ser	Ala	Ala	Trp	Asn	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Arg	Gly	Leu	Glu
		35					40					45			
Trp	Leu	Gly	Arg	Thr	Tyr	Tyr	Arg	Ser	Lys	Trp	Tyr	Asn	Asp	Tyr	Ala
		50				55					60				
Val	Ser	Val	Lys	Ser	Arg	Ile	Thr	Ile	Asn	Pro	Asp	Thr	Ser	Lys	Asn
					70					75					80
Gln	Phe	Ser	Leu	Gln	Leu	Asn	Ser	Val	Thr	Pro	Glu	Asp	Thr	Ala	Val
				85					90					95	
Tyr	Tyr	Cys	Ala	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser					
			115					120							

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..327
(D) OTHER INFORMATION: /product= "V kappa 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GAT	ATC	CAG	ATG	ACC	CAG	AGC	CCG	TCT	AGC	CTG	AGC	GCG	AGC	GTG	GGT	48
Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5				10						15		
GAT	CGT	GTG	ACC	ATT	ACC	TGC	AGA	GCG	AGC	CAG	GGC	ATT	AGC	AGC	TAT	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	Tyr	
			20					25					30			
CTG	GCG	TGG	TAC	CAG	CAG	AAA	CCA	GGT	AAA	GCA	CCG	AAA	CTA	TTA	ATT	144
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
TAT	GCA	GCC	AGC	AGC	TTG	CAA	AGC	GGG	GTC	CCG	TCC	CGT	TTT	AGC	GGC	192
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55				60						
TCT	GGA	TCC	GGC	ACT	GAT	TTT	ACC	CTG	ACC	ATT	AGC	AGC	CTG	CAA	CCT	240
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65				70				75						80		
GAA	GAC	TTT	GCG	ACC	TAT	TAT	TGC	CAG	CAG	CAT	TAT	ACC	ACC	CCG	CCG	288
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr	Pro	Pro	
				85				90						95		
ACC	TTT	GGC	CAG	GGT	ACG	AAA	GTT	GAA	ATT	AAA	CGT	ACG				327
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr				
			100					105								

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	Tyr
			20					25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65				70				75						80	
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr	Pro	Pro

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..342
- (D) OTHER INFORMATION: /product= "V kappa 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAT ATC GTG ATG ACC CAG AGC CCA CTG AGC CTG CCA GTG ACT CCG GGC	48
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly	
110 115 120 125	
GAG CCT GCG AGC ATT AGC TGC AGA AGC AGC CAA AGC CTG CTG CAT AGC	96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser	
130 135 140	
AAC GGC TAT AAC TAT CTG GAT TGG TAC CTT CAA AAA CCA GGT CAA AGC	144
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
145 150 155	
CCG CAG CTA TTA ATT TAT CTG GGC AGC AAC CGT GCC AGT GGG GTC CCG	192
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro	
160 165 170	
GAT CGT TTT AGC GGC TCT GGA TCC GGC ACC GAT TTT ACC CTG AAA ATT	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
175 180 185	
AGC CGT GTG GAA GCT GAA GAC GTG GGC GTG TAT TAT TGC CAG CAG CAT	288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln His	
190 195 200 205	
TAT ACC ACC CCG CCG ACC TTT GGC CAG GGT ACG AAA GTT GAA ATT AAA	336
Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
210 215 220	
CGT ACG	
342	

Arg Thr

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln His
85 90 95
Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..330
- (D) OTHER INFORMATION: /product= "V kappa 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GAT	ATC	GTG	CTG	ACC	CAG	AGC	CCG	GCG	ACC	CTG	AGC	CTG	TCT	CCG	GGC	48
Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
115					120					125					130	
GAA	CGT	GCG	ACC	CTG	AGC	TGC	AGA	GCG	AGC	CAG	AGC	GTG	AGC	AGC	AGC	96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser	
				135					140					145		
TAT	CTG	GCG	TGG	TAC	CAG	CAG	AAA	CCA	GGT	CAA	GCA	CCG	CGT	CTA	TTA	144
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	
			150					155						160		
ATT	TAT	GGC	GCG	AGC	AGC	CGT	GCA	ACT	GGG	GTC	CCG	GCG	CGT	TTT	AGC	192
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	
		165					170					175				
GGC	TCT	GGA	TCC	GGC	ACG	GAT	TTT	ACC	CTG	ACC	ATT	AGC	AGC	CTG	GAA	240
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	
	180					185					190					
CCT	GAA	GAC	TTT	GCG	GTG	TAT	TAT	TGC	CAG	CAG	CAT	TAT	ACC	ACC	CCG	288
Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	His	Tyr	Thr	Thr	Pro	
195					200					205					210	
CCG	ACC	TTT	GGC	CAG	GGT	ACG	AAA	GTT	GAA	ATT	AAA	CGT	ACG			330
Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr			
			215						220							

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser
	50				55					60					
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu
65					70					75					80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic gene"

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..345
(D) OTHER INFORMATION: /product= "v kappa 4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GAT ATC GTG ATG ACC CAG AGC CCG GAT AGC CTG GCG GTG AGC CTG GGC	48
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly	
115 120 125	
GAA CGT GCG ACC ATT AAC TGC AGA AGC AGC CAG AGC GTG CTG TAT AGC	96
Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser	
130 135 140	
AGC AAC AAC AAA AAC TAT CTG GCG TGG TAC CAG CAG AAA CCA GGT CAG	144
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
145 150 155	
CCG CCG AAA CTA TTA ATT TAT TGG GCA TCC ACC CGT GAA AGC GGG GTC	192
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
160 165 170	
CCG GAT CGT TTT AGC GGC TCT GGA TCC GGC ACT GAT TTT ACC CTG ACC	240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr	
175 180 185 190	
ATT TCG TCC CTG CAA GCT GAA GAC GTG GCG GTG TAT TAT TGC CAG CAG	288
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln	
195 200 205	
CAT TAT ACC ACC CCG CCG ACC TTT GGC CAG GGT ACG AAA GTT GAA ATT	336
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
210 215 220	
AAA CGT ACG	345

Lys Arg Thr
225

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15
Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30
Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95
His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110
Lys Arg Thr
115

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..327
- (D) OTHER INFORMATION: /product= "V lambda 1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CAG AGC GTG CTG ACC CAG CCG CCT TCA GTG AGT GGC GCA CCA GGT CAG	48
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln	
120 125 130	
CGT GTG ACC ATC TCG TGT AGC GGC AGC AGC AGC AAC ATT GGC AGC AAC	96
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn	
135 140 145	
TAT GTG AGC TGG TAC CAG CAG TTG CCC GGG ACG GCG CCG AAA CTG CTG	144
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu	
150 155 160	
ATT TAT GAT AAC AAC CAG CGT CCC TCA GGC GTG CCG GAT CGT TTT AGC	192
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser	
165 170 175	
GGA TCC AAA AGC GGC ACC AGC GCG AGC CTT GCG ATT ACG GGC CTG CAA	240
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln	
180 185 190 195	
AGC GAA GAC GAA GCG GAT TAT TAT TGC CAG CAG CAT TAT ACC ACC CCG	288
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro	
200 205 210	
CCT GTG TTT GGC GGC GGC ACG AAG TTA ACC GTT CTT GGC	327
Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly	
215 220	

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln	
1 5 10 15	
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn	
20 25 30	
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu	
35 40 45	
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser	
50 55 60	
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln	
65 70 75 80	

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
85 90 95

Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 330 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic gene"

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..330
(D) OTHER INFORMATION: /product= "V lambda 2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

CAG AGC GCA CTG ACC CAG CCA GCT TCA GTG AGC GGC TCA CCA GGT CAG	48
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln	
110 115 120 125	
AGC ATT ACC ATC TCG TGT ACG GGT ACT AGC AGC GAT GTG GGC GGC TAT	96
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr	
130 135 140	
AAC TAT GTG AGC TGG TAC CAG CAG CAT CCC GGG AAG GCG CCG AAA CTG	144
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu	
145 150 155	
ATG ATT TAT GAT GTG AGC AAC CGT CCC TCA GGC GTG AGC AAC CGT TTT	192
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe	
160 165 170	
AGC GGA TCC AAA AGC GGC AAC ACC GCG AGC CTG ACC ATT AGC GGC CTG	240
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu	
175 180 185	
CAA GCG GAA GAC GAA GCG GAT TAT TAT TGC CAG CAG CAT TAT ACC ACC	288
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr	
190 195 200 205	
CCG CCT GTG TTT GGC GGC GGC ACG AAG TTA ACC GTT CTT GGC	330
Pro Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly	
210 215	

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr
85 90 95
Pro Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..321
(D) OTHER INFORMATION: /product= "V lambda 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

AGC TAT GAA CTG ACC CAG CCG CCT TCA GTG AGC GTT GCA CCA GGT CAG
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
115 120 125

48

ACC GCG CGT ATC TCG TGT AGC GGC GAT GCG CTG GGC GAT AAA TAC GCG	96
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala	
130 135 140	
AGC TGG TAC CAG CAG AAA CCC GGG CAG GCG CCA GTT CTG GTG ATT TAT	144
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr	
145 150 155	
GAT GAT TCT GAC CGT CCC TCA GGC ATC CCG GAA CGC TTT AGC GGA TCC	192
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser	
160 165 170	
AAC AGC GGC AAC ACC GCG ACC CTG ACC ATT AGC GGC ACT CAG GCG GAA	240
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu	
175 180 185 190	
GAC GAA GCG GAT TAT TAT TGC CAG CAG CAT TAT ACC ACC CCG CCT GTG	288
Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Val	
195 200 205	
TTT GGC GGC GGC ACG AAG TTA ACC GTT CTT GGC	321
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly	
210 215	

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln	1 5 10 15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala	20 25 30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr	35 40 45
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser	50 55 60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu	65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Val	85 90 95
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly	100 105

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: /product= "VH1A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

CAG GTG CAA TTG GTT CAG TCT GGC GCG GAA GTG AAA AAA CCG GGC AGC	48
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser	
110 115 120	
AGC GTG AAA GTG AGC TGC AAA GCC TCC GGA GGC ACT TTT AGC AGC TAT	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr	
125 130 135	
GCG ATT AGC TGG GTG CGC CAA GCC CCT GGG CAG GGT CTC GAG TGG ATG	144
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
140 145 150 155	
GGC GGC ATT ATT CCG ATT TTT GGC ACG GCG AAC TAC GCG CAG AAG TTT	192
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe	
160 165 170	
CAG GGC CGG GTG ACC ATT ACC GCG GAT GAA AGC ACC AGC ACC GCG TAT	240
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr	
175 180 185	
ATG GAA CTG AGC AGC CTG CGT AGC GAA GAT ACG GCC GTG TAT TAT TGC	288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys	
190 195 200	
GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC CAA	336
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln	
205 210 215	
GGC ACC CTG GTG ACG GTT AGC TCA G	361
Gly Thr Leu Val Thr Val Ser Ser	
220 225	

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: /product= "VH1B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CAG GTG CAA TTG GTT CAG AGC GGC GCG GAA GTG AAA AAA CCG GGC GCG
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
125 130 135

48

AGC	GTG	AAA	GTG	AGC	TGC	AAA	GCC	TCC	GGA	TAT	ACC	TTT	ACC	AGC	TAT	96
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	
			140					145					150			
TAT	ATG	CAC	TGG	GTC	CGC	CAA	GCC	CCT	GGG	CAG	GGT	CTC	GAG	TGG	ATG	144
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		155					160					165				
GGC	TGG	ATT	AAC	CCG	AAT	AGC	GGC	GGC	ACG	AAC	TAC	GCG	CAG	AAG	TTT	192
Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	
	170					175					180					
CAG	GGC	CGG	GTG	ACC	ATG	ACC	CGT	GAT	ACC	AGC	ATT	AGC	ACC	GCG	TAT	240
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr	
185					190					195				200		
ATG	GAA	CTG	AGC	AGC	CTG	CGT	AGC	GAA	GAT	ACG	GCC	GTG	TAT	TAT	TGC	288
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			205					210				215				
GCG	CGT	TGG	GGC	GGC	GAT	GGC	TTT	TAT	GCG	ATG	GAT	TAT	TGG	GGC	CAA	336
Ala	Arg	Trp	Gly	Gly	Asp	Gly	Phe	Tyr	Ala	Met	Asp	Tyr	Trp	Gly	Gln	
		220					225						230			
GGC	ACC	CTG	GTG	ACG	GTT	AGC	TCA	G								361
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
		235				240										

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	
		20					25					30				
Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35				40						45				
Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	
	50					55					60					
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr	
	65				70					75					80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	

85 90 95

Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..363
- (D) OTHER INFORMATION: /product= "VH2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

CAG GTG CAA TTG AAA GAA AGC GGC CCG GCC CTG GTG AAA CCG ACC CAA	48
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln	
125 130 135	
ACC CTG ACC CTG ACC TGT ACC TTT TCC GGA TTT AGC CTG TCC ACG TCT	96
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser	
140 145 150	
GGC GTT GGC GTG GGC TGG ATT CGC CAG CCG CCT GGG AAA GCC CTC GAG	144
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu	
155 160 165	
TGG CTG GCT CTG ATT GAT TGG GAT GAT GAT AAG TAT TAT AGC ACC AGC	192
Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser	
170 175 180	
CTG AAA ACG CGT CTG ACC ATT AGC AAA GAT ACT TCG AAA AAT CAG GTG	240
Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val	
185 190 195 200	
GTG CTG ACT ATG ACC AAC ATG GAC CCG GTG GAT ACG GCC ACC TAT TAT	288
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr	
205 210 215	
TGC GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC	336
Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly	
220 225 230	

CAA GGC ACC CTG GTG ACG GTT AGC TCA G
 Gln Gly Thr Leu Val Thr Val Ser Ser
 235 240

364

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60
 Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..360
- (D) OTHER INFORMATION: /product= "VH3"

2157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GAA GTG CAA TTG GTG GAA AGC GGC GGC GGC CTG GTG CAA CCG GGC GGC	48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
125 130 135	
AGC CTG CGT CTG AGC TGC GCG GCC TCC GGA TTT ACC TTT AGC AGC TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
140 145 150	
GCG ATG AGC TGG GTG CGC CAA GCC CCT GGG AAG GGT CTC GAG TGG GTG	144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
155 160 165	
AGC GCG ATT AGC GGT AGC GGC GGC AGC ACC TAT TAT GCG GAT AGC GTG	192
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val	
170 175 180 185	
AAA GGC CGT TTT ACC ATT TCA CGT GAT AAT TCG AAA AAC ACC CTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
190 195 200	
CTG CAA ATG AAC AGC CTG CGT GCG GAA GAT ACG GCC GTG TAT TAT TGC	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
205 210 215	
GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC CAA	336
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln	
220 225 230	
GGC ACC CTG GTG ACG GTT AGC TCA G	361
Gly Thr Leu Val Thr Val Ser Ser	
235 240	

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	

258

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic gene"

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..357
(D) OTHER INFORMATION: /product= "VH4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

CAG GTG CAA TTG CAA GAA AGT GGT CCG GGC CTG GTG AAA CCG AGC GAA	48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu	
125 130 135	
ACC CTG AGC CTG ACC TGC ACC GTT TCC GGA GGC AGC ATT AGC AGC TAT	96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr	
140 145 150	
TAT TGG AGC TGG ATT CGC CAG CCG CCT GGG AAG GGT CTC GAG TGG ATT	144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile	
155 160 165	
GGC TAT ATT TAT TAT AGC GGC AGC ACC AAC TAT AAT CCG AGC CTG AAA	192
Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys	
170 175 180	
AGC CGG GTG ACC ATT AGC GTT GAT ACT TCG AAA AAC CAG TTT AGC CTG	240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu	
185 190 195 200	

AAA CTG AGC AGC GTG ACG GCG GCG GAT ACG GCC GTG TAT TAT TGC GCG 288
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 205 210 215
 CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC CAA GCG 336
 Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 220 225 230
 ACC CTG GTG ACG GTT AGC TCA G 358
 Thr Leu Val Thr Val Ser Ser
 235

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

260

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:1..360
 (D) OTHER INFORMATION:/product= "VH5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAA GTG CAA TTG GTT CAG AGC GGC GCG GAA GTG AAA AAA CCG GGC GAA	48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu	
120 125 130 135	
AGC CTG AAA ATT AGC TGC AAA GGT TCC GGA TAT TCC TTT ACG AGC TAT	96
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr	
140 145 150	
TGG ATT GGC TGG GTG CGC CAG ATG CCT GGG AAG GGT CTC GAG TGG ATG	144
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met	
155 160 165	
GGC ATT ATT TAT CCG GGC GAT AGC GAT ACC CGT TAT TCT CCG AGC TTT	192
Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe	
170 175 180	
CAG GGC CAG GTG ACC ATT AGC GCG GAT AAA AGC ATT AGC ACC GCG TAT	240
Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr	
185 190 195	
CTT CAA TGG AGC AGC CTG AAA GCG AGC GAT ACG GCC ATG TAT TAT TGC	288
Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys	
200 205 210 215	
GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT TGG GGC CAA	336
Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln	
220 225 230	
GGC ACC CTG GTG ACG GTT AGC TCA G	361
Gly Thr Leu Val Thr Val Ser Ser	
235	

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..369
- (D) OTHER INFORMATION: /product= "VH6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CAG GTG CAA TTG CAA CAG TCT GGT CCG GGC CTG GTG AAA CCG AGC CAA	48
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln	
125 130 135	
ACC CTG AGC CTG ACC TGT GCG ATT TCC GGA GAT AGC GTG AGC AGC AAC	96
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn	
140 145 150	
AGC GCG GCG TGG AAC TGG ATT CGC CAG TCT CCT GGG CGT GGC CTC GAG	144
Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu	
155 160 165	

TGG CTG GGC CGT ACC TAT TAT CGT AGC AAA TGG TAT AAC GAT TAT GCG	192
Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala	
170 175 180	
GTG AGC GTG AAA AGC CGG ATT ACC ATC AAC CCG GAT ACT TCG AAA AAC	240
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn	
185 190 195 200	
CAG TTT AGC CTG CAA CTG AAC AGC GTG ACC CCG GAA GAT ACG GCC GTG	288
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val	
205 210 215	
TAT TAT TGC GCG CGT TGG GGC GGC GAT GGC TTT TAT GCG ATG GAT TAT	336
Tyr Tyr Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr	
220 225 230	
TGG GGC CAA GGC ACC CTG GTG ACG GTT AGC TCA G	370
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
235 240	

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln	
1 5 10 15	
Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn	
20 25 30	
Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu	
35 40 45	
Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala	
50 55 60	
Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn	
65 70 75 80	
Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val	
85 90 95	
Tyr Tyr Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr	
100 105 110	
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
115 120	

263

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GAATGCATAC GCTGATATCC AGATGACCCA GAGCCCGTCT AGCCTGAGC

49

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CGCTCTGCAG GTAATGGTCA CACGATCACC CACGCTCGCG CTCAGGCTAG ACGGGC
56

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GACCATACC TGCAGAGCGA GCCAGGGCAT TAGCAGCTAT CTGGCGTGGT ACCAGCAG
58

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CTTTGCAAGC TGCTGGCTGC ATAAATTAAT AGTTTCGGTG CTTTACCTGG TTTCTGCTGG 60
TACCACGCCA G 71

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

CAGCCAGCAG CTTGCAAAGC GGGGTCCCGT CCGTTTTTCG CGGCTCTGGA TCCGGCACTG 60
ATTTTAC 67

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GATAATAGGT CGCAAAGTCT TCAGGTTGCA GGCTGCTAAT GGTCAGGGTA AAATCAGTGC 60
CGGATCC 67

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CGATATCGTG ATGACCCAGA GCCCACTGAG CCTGCCAGTG ACTCCGGGCG AGCC 54

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GCCGTTGCTA TGCAGCAGGC TTTGGCTGCT TCTGCAGCTA ATGCTCGCAG GCTCGCCCCG 60
AGTCAC 66

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CTGCTGCATA GCAACGGCTA TAACTATCTG GATTGGTACC TTCAAAAACC AGGTCAAAGC 60
CC 62

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CGATCCGGGA CCCACTGGC ACGGTGCTG CCCAGATAAA TTAATAGCTG CGGGCTTTGA 60
CCTGGTTTTT G 71

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

AGTGGGGTCC CGGATCGTTT TAGCGGCTCT GGATCCGGCA CCGATTTTAC CCTGAAAATT 60
AGCCGTGTG 69

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide".

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCATGCAATA ATACAGCCCC ACGTCTTCAG CTTCCACACG GCTAATTTTC AGGG

54

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

GAATGCATAC GCTGATATCG TGCTGACCCA'GAGCCCCG

38

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGCTCTGCAG CTCAGGGTCG CACGTTCGCC CGGAGACAGG CTCAGGGTCG CCGGGCTCTG
GGTCAGC

60
67

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CCCTGAGCTG CAGAGCGAGC CAGAGCGTGA GCAGCAGCTA TCTGGCGTGG TACCAG 56

- (2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GCACGGCTGC TCGCGCCATA AATTAATAGA CGCGGTGCTT GACCTGGTTT CTGCTGGTAC 60

CACGCCAGAT AG 72

- (2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GCGCGAGCAG CCGTGCAACT GGGGTCCCGG CGCGTTTGTAG CGGCTCTGGA TCCGGCACGG 60

ATTTTAC 67

- (2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GATAATACAC CGCAAAGTCT TCAGGTTCCA GGCTGCTAAT GGTCAGGGTA AAATCCGTGC 60
CGGATC 66

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GAATGCATAC GCTGATATCG TGATGACCCA GAGCCCGGAT AGCCTGGCG 49

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GCTTCTGCAG TTAATGGTCG CACGTTGCC CAGGCTCACC GCCAGGCTAT CCGGGC 56

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CGACCATTAA CTGCAGAAGC AGCCAGAGCG TGCTGTATAG CAGCAACAAC AAAAATATC 60
TGGCGTGGTA CCAG 74

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GATGCCCAAT AAATTAATAG TTTCGGCGGC TGACCTGGTT TCTGCTGGTA CCACGCCAGA 60
TAG 63

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

AAACTATTAA TTTATTGGGC ATCGACCCGT GAAAGCGGGG TCCCGGATCG TTTAGCGGC 60
TCTGGATCCG GCAC 74

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GATAATACAC CGCCACGTCT TCAGCTTGCA GGGACGAAAT GGTCAGGGTA AAATCAGTGC 60
CGGATCCAGA GCC 73

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GAATGCATAC GCTCAGAGCG TGCTGACCCA GCCGCCTTCA GTGAGTGG 48

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

CAATGTTGCT GCTGCTGCCG CTACACGAGA TGGTCACACG CTGACCTGGT GCGCCACTCA 60

CTGAAGGCGG C

71

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

GGCAGCAGCA GCAACATTGG CAGCAACTAT GTGAGCTGGT ACCAGCAGTT GCCCGGGAC 59

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGGCACGCC TGAGGGACGC TGGTTGTTAT CATAAATCAG CAGTTTCGGC GCCGTCCCGG 60
GCAACTGC 68

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCCTCAGGCG TGCCGGATCG TTTTAGCGGA TCCAAAAGCG GCACCAGCGC GAGCCTTGCG 60

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCGCTTCGTC TTCGCTTTC AGGCCCGTAA TCGCAAGGCT CGCGCTGG 48

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

GAATGCATAC GCTCAGAGCG CACTGACCCA GCCAGCTTCA GTGAGCGGC 49

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CGCTGCTAGT ACCCGTACAC GAGATGGTAA TGCTCTGACC TGGTGAGCCG CTCACTGAAG 60
CTGG 64

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

GTACGGGTAC TAGCAGCGAT GTGGGCGGCT ATA ACTATGT GAGCTGGTAC CAGCAGCATC 60
CCGG 64

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CGCCTGAGGG ACGGTTGCTC ACATCATAAA TCATCAGTTT CGGCGCCTTC CCGGGATGCT 60
GCTGGTAC 68

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CAACCGTCCC TCAGCGGTGA GCAACCGTTT TAGCGGATCC AAAAGCGGCA ACACCGCGAG 60
CC 62

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGCTTCGTC TTCCGCTTGC AGGCCGCTAA TGGTCAGGCT CGCGGTGTTG CCG 53

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GAATGCATAC GCTAGCTATG AACTGACCCA GCCGCCTTCA GTGAGCG 47

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

CGCCCAGCGC ATCGCCGCTA CACGAGATAC GCGCGGTCTG ACCTGGTGCA ACGCTCACTG 60
AAGGCGGC 68

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCGATGCGC TGGGCGATAA ATACGCGAGC TGGTACCAGC AGAAACCCGG GCAGGCGC 58

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GCGTTCCGGG ATGCCTGAGG GACGGTCAGA ATCATCATAA ATCACCAGAA CTGGCGCCTG 60
CCCGGGTTTC 70

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

CAGGCATCCC GGAACGCTTT AGCGGATCCA ACAGCGGCAA CACCGCGACC CTGACCATTA 60
GCGG 64

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGCTTCGTC TTCCGCCTGA GTGCCGCTAA TGGTCAGGGT C 41

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GCTCTTCACC CCTGTTACCA AAGCCCAGGT GCAATTG 37

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

GGCTTTGCAG CTCAC TTCA CGCTGCTGCC CGGTTTTTTC ACTTCCGCGC CAGACTGAAC 60
CAATTGCACC TGGGCTTTG 79

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

GAAAGTGAGC TGCAAAGCCT CCGGAGGCAC TTTTAGCAGC TATGCGATTA GCTGGGTGCG 60
CCAAGCCCCT GGGCAGGGTC 80

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GCCCTGAAAC TTCTGCGCGT AGTTCGCCGT GCCAAAAATC GGAATAATGC CGCCCATCCA 60
CTCGAGACCC TGCCAGGGG C 81

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GCGCAGAAAGT TTCAGGGCCG GGTGACCATT ACCGCGGATG AAAGCACCAG CACCGCGTAT 60
ATGGAAGTGA GCAGCCTGCG 80

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCGCGCAATA ATACACGGCC GTATCTTCGC TACGCAGGCT GTCAGTTCC 50

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

GGCTTTGCAG CTCACCTTTCA CGCTCGCGCC CGGTTTTTTC ACTTCCGCGC CGCTCTGAAC 60
CAATTGCACC TGGGCTTTG 79

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

GAAAGTGAGC TGCAAAGCCT CCGGATATAC CTTTACCAGC TATTATATGC ACTGGGTCCG 60
CCAAGCCCCT GGGCAGGGTC 80

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GCCCTGAAAC TTCTGCGCGT AGTTCGTGCC GCCGCTATTC GGGTTAATCC AGCCCATCCA 60
CTCGAGACCC TGCCCAGGGG C 81

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

GCGCAGAAGT TTCAGGGCCG GGTGACCATG ACCCGTGATA CCAGCATTAG CACCGCGTAT 60
 ATGGAAGTGA GCAGCCTGCG 80

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GGTACAGGTC AGGGTCAGGG TTTGGGTCGG TTCACCAGG GCCGGGCCGC TTTCTTTCAA 60
 TTGCACCTGG GCTTTG 76

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

CTGACCCTGA CCTGTACCTT TTCGGATTT AGCCTGTCCA CGTCTGGCGT TGGCGTGGGC 60
 TGGATTCGCC AGCCGCCTGG GAAAG 85

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GCGTTTTTCAG GCTGGTGCTA TAATACTTAT CATCATCCCA ATCAATCAGA GCCAGCCACT 60
CGAGGGCTTT CCCAGGCGGC TGG 83

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GCACCAGCCT GAAAACGCGT CTGACCATTA GCAAAGATAC TTCGAAAAAT CAGGTGGTGC 60
TGACTATGAC CAACATGG 78

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GCGCGCAATA ATAGGTGGCC GTATCCACCG GGTCCATGTT GGTCATAGTC AGC 53

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

CGAAGTGCAA TTGGTGAAA GCGGCGGCGG CCTGGTGCAA CCGGGCGGCA G

51

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CATAGCTGCT AAAGGTAAAT CCGGAGGCCG CGCAGCTCAG ACGCAGGCTG CCGCCCGGTT

60

GCAC

64

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GATTACCTT TAGCAGCTAT GCGATGAGCT GGGTGCGCCA AGCCCCTGGG AAGGGTCTCG

60

AGTGGGTGAG

70

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

GGCCTTTCAC GCTATCCGCA TAATAGGTGC TGCCGCCGCT ACCGCTAATC GCGCTCACCC 60

ACTCGAGACC C 71

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CGGATAGCGT GAAAGGCCGT TTTACCATT CACGTGATAA TCGAAAAAC ACCCTGTATC 60

TGCAAATGAA CAG 73

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

CACGCGCGCA ATAATACAG GCCGTATCTT CCGCACGCAG GCTGTTTCATT TGCAGATACA 60

GG 62

(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

GGTCAGGCTC AGGTTTCGC TCGTTTCAC CAGGCCGGA CCACTTCTT GCAATTGCAC 60
CTGGGCTTTG 70

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

GAAACCCTGA GCCTGACCTG CACCGTTTCC GGAGGCAGCA TTAGCAGCTA TTATTGGAGC 60
TGGATTGCGC AGCCGC 76

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

GATTATAGTT GGTGCTGCCG CTATAATAAA TATAGCCAAT CCACTCGAGA CCCTTCCCAG 60

GCGGCTGGCG AATCCAG

77

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CGGCAGCACC AACTATAATC CGAGCCTGAA AAGCCGGGTG ACCATTAGCG TTGATACTTC 60

GAAAAACCAG TTTAGCCTG

79

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GCGCGCAATA ATACACGGCC GTATCCGCCG CCGTCACGCT GCTCAGTTTC AGGCTAAACT 60

GGTTTTTCG

69

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

GCTCTTCACC CCTGTTACCA AAGCCGAAGT GCAATTG

37

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CCTTTGCAGC TAATTTTCAG GCTTTGCCCC GGTTTTTCA CTTCGCGCC GCTCTGAACC 60

AATTGCACTT CGGCTTTGG

79

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CCTGAAAATT AGCTGCAAAG GTTCCGGATA TTCTTTACG AGCTATTGGA TTGGCTGGGT 60

GCGCCAGATG CCTGG

75

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

CGGAGAATAA CGGGTATCGC TATCGCCCGG ATAAATAATG CCCATCCACT CGAGACCCTT 60
CCCAGGCATC TGGCGCAC 78

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CGATACCCGT TATTCTCCGA GCTTTCAGGG CCAGGTGACC ATTAGCGCGG ATAAAAGCAT 60
TAGCACCGCG TATCTTC 77

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

GCGCGCAATA ATACATGGCC GTATCGCTCG CTTTCAGGCT GCTCCATTGA AGATACGCGG 60
TGCTAATG 68

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

GAAATCGCAC AGGTCAGGCT CAGGGTTTGG CTCGGTTTCA CCAGGCCCGG ACCAGACTGT 60
TGCAATTGCA CCTGGGCTTT G 81

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

GCCTGACCTG TGCATTTCG GGAGATAGCG TGAGCAGCAA CAGCGCGGCG TGGAAGTGA 60
TTCGCCAGTC TCCTGGGCG 79

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CACCGCATAA TCATTATACC ATTTGCTACG ATAATAGGTA CGGCCAGCC ACTCGAGGCC 60
ACGCCAGGA GACTGGCG 78

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

GGTATAACGA TTATGCGGTG AGCGTGAAAA GCCGGATTAC CATCAACCCG GATACTTCGA 60
 AAAACCAAGTT TAGCCTGC 78

- (2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

GCGCGCAATA ATACACGGCC GTATCTTCG GGGTCACGCT GTTCAGTTGC AGGCTAACT 60
 GGTTTTTC
 68

- (2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

GGCTGAAGAC GTGGGCGTGT ATTATTGCCA GCAGCATTAT ACCACCCCGC CGACCTTTGG 60

CCAGGGTAC

69

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

GCGGAAAAAT AAACACGCTC GGAGCAGCCA CCGTACGTTT AATTTCAACT TTCGTACCCT 60

GGCCAAAGGT C

71

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

GAGCGTGTTT ATTTTCCGC CGAGCGATGA ACAACTGAAA AGCGGCACGG CGAGCGTGGT 60

GTGCCTGCTG

70

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

CAGCGCGTTG TCTACTTTCC ACTGAACTTT CGCTTCACGC GGATAAAAGT TGTTCAGCAG 60
GCACACCACG C 71

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

GAAAGTAGAC AACGCGCTGC AAAGCGGCAA CAGCCAGGAA AGCGTGACCG AACAGGATAG 60
CAAAGATAG 69

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

GTTTTTCATA ATCCGCTTTG CTCAGGGTCA GGGTGCTGCT CAGAGAATAG GTGCTATCTT 60
TGCTATCCTG TTCG 74

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

GCAAAGCGGA TTATGAAAAA CATAAAGTGT ATGCGTGCGA AGTGACCCAT CAAGGTCTGA 60
GCAGCCCGGT G 71

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

GGCATGCTTA TCAGGCTCG CCACGATTAA AAGATTTAGT CACCGGGCTG CTCAGAC 57

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GGCGTCTAGA GGCCAAGGCA CCCTGGTGAC GGTTAGCTCA GCGTCGAC 48

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GTGCTTTTGC TGCTCGGAGC CAGCGGAAAC ACGCTTGGAC CTTTGGTCGA CGCTGAGCTA 60
ACC 63

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CTCCGAGCAG CAAAAGCACC AGCGGCGGCA CGGCTGCCCT GGGCTGCCTG GTTAAAGATT 60
ATTTC 66

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

CTGGTCAGCG CCCCGCTGTT CCAGCTCAGC GTGACTGGTT CCGGGAAATA ATCTTTAACC 60
AGGCA 65

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AGCGGGGCGC TGACCAGCGG CGTGCATACC TTTCCGGCGG TGCTGCAAAG CAGCGGCCTG 60

- (2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GTGCCTAAGC TGCTGCTCGG CACGGTCACA ACCTGCTCA GGCTATACAG GCCGCTGCTT 60

TGCAG 65

- (2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

GAGCAGCAGC TTAGGCACTC AGACCTATAT TTGCAACGTG AACCATAAAC CGAGCAACAC 60

C

61

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCGCGAATTC GCTTTTCGGT TCCACTTTT TATCCACTTT GGTGTTGCTC GGTTTATGG . 59

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic gene"

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 7..321
 (D) OTHER INFORMATION: /product= "C kappa"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CGTACG GTG GCT GCT CCG AGC GTG TTT ATT TTT CCG CCG AGC GAT GAA	48
Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu	
125 130 135	
CAA CTG AAA AGC GGC ACG GCG AGC GTG GTG TGC CTG CTG AAC AAC TTT	96
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe	
140 145 150	
TAT CCG CGT GAA GCG AAA GTT CAG TGG AAA GTA GAC AAC GCG CTG CAA	144
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln	
155 160 165	
AGC GGC AAC AGC CAG GAA AGC GTG ACC GAA CAG GAT AGC AAA GAT AGC	192
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser	
170 175 180 185	
ACC TAT TCT CTG AGC AGC ACC CTG ACC CTG AGC AAA GCG GAT TAT GAA	240

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
190 195 200

AAA CAT AAA GTG TAT GCG TGC GAA GTG ACC CAT CAA GGT CTG AGC AGC 288
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
205 210 215

CCG GTG ACT AAA TCT TTT AAT CGT GGC GAG GCC TGATAAGCAT GC 333
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ala
220 225

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
1 5 10 15

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
20 25 30

Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly
35 40 45

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
50 55 60

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
65 70 75 80

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
85 90 95

Thr Lys Ser Phe Asn Arg Gly Glu Ala
100 105

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 6..317
- (D) OTHER INFORMATION: /product= "CH1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```
GCTCA GCG TCG ACC AAA GGT CCA AGC GTG TTT CCG CTG GCT CCG AGC 47
    Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
                        110                        115

AGC AAA AGC ACC AGC GGC GGC ACG GCT GCC CTG GGC TGC CTG GTT AAA 95
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
120                        125                        130                        135

GAT TAT TTC CCG GAA CCA GTC ACC GTG AGC TGG AAC AGC GGG GCG CTG 143
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
                        140                        145                        150

ACC AGC GGC GTG CAT ACC TTT CCG GCG GTG CTG CAA AGC AGC GGC CTG 191
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                        155                        160                        165

TAT AGC CTG AGC AGC GTT GTG ACC GTG CCG AGC AGC AGC TTA GGC ACT 239
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
                        170                        175                        180

CAG ACC TAT ATT TGC AAC GTG AAC CAT AAA CCG AGC AAC ACC AAA GTG 287
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
185                        190                        195

GAT AAA AAA GTG GAA CCG AAA AGC GAA TTC TGATAAGCTT 327
Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
200                        205
```

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1          5          10          15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
          20          25          30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35          40          45
```

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Glu Phe
100

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 85..396
- (D) OTHER INFORMATION: /product= "C lambda"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

GAAGACGAAG CGGATTATTA TTGCCAGCAG CATTATACCA CCCCGCCTGT GTTTGGCGGC 60

GGCACGAAGT TAACCGTTCT TGGC CAG CCG AAA GCC GCA CCG AGT GTG ACG 111
Gln Pro Lys Ala Ala Pro Ser Val Thr
105 110

CTG TTT CCG CCG AGC AGC GAA GAA TTG CAG GCG AAC AAA GCG ACC CTG 159
Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu
115 120 125

GTG TGC CTG ATT AGC GAC TTT TAT CCG GGA GCC GTG ACA GTG GCC TGG 207
Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp
130 135 140 145

AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC 255
Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro
150 155 160

TCC AAA CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAT CTG AGC CTG 303
Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu
165 170 175

ACG CCT GAG CAG TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG 351

Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr
180 185 190

CAT GAG GGG AGC ACC GTG GAA AAA ACC GTT GCG CCG ACT GAG GCC 396
His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Ala
195 200 205

TGATAAGCAT GC 408

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
1 5 10 15

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
20 25 30

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
35 40 45

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
50 55 60

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
65 70 75 80

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
85 90 95

Lys Thr Val Ala Pro Thr Glu Ala
100

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GAAGACAAGC GGATTATTAT TGCCAGCAGC ATTATACCAC CCGCCTGTG TTTGGCGGCG 60
GCACGAAGTT AACCGTTC 78

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CAATTCTTCG CTGCTCGGCG GAAACAGCGT CACACTCGGT GCGGCTTTCG GCTGGCCAAG 60
AACGGTTAAC TTCGTGCCGC 80

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCCGAGCAG CGAAGAATTG CAGGCGAACA AAGCGACCCT GGTGTGCCTG ATTAGCGACT 60
TTTATCCGGG AGCCGTGACA 80

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

TGTTTGGAGG GTGTGGTGGT CTCCACTCCC GCCTTGACGG GGCTGCTATC TGCCTTCCAG 60
GCCACTGTCA CGGCTCCCGG 80

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

CCACACCCCTC CAAACAAAGC AACAAACAAGT ACGCGGCCAG CAGCTATCTG AGCCTGACGC 60
CTGAGCAGTG GAAGTCCCAC AGAAGCTACA GCTG 94

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

GCATGCTTAT CAGGCCTCAG TCGGCGCAAC GGTTTTTTCC ACGGTGCTCC CCTCATGCGT 60
GACCTGGCAG CTGTAGCTTC 80

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 843 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic gene"

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..843
 (D) OTHER INFORMATION: /product= "VH3-Vk2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ATG AAA CAA AGC ACT ATT GCA CTG GCA CTC TTA CCG TTG CTC TTC ACC	48
Met Lys Gln Ser Thr Ile Ala Leu Ala Leu Leu Pro Leu Leu Phe Thr	
105 110 115 120	
CCT GTT ACC AAA GCC GAC TAC AAA GAT GAA GTG CAA TTG GTG GAA AGC	96
Pro Val Thr Lys Ala Asp Tyr Lys Asp Glu Val Gln Leu Val Glu Ser	
125 130 135	
GGC GGC GGC CTG GTG CAA CCG GGC GGC AGC CTG CGT CTG AGC TGC GCG	144
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala	
140 145 150	
GCC TCC GGA TTT ACC TTT AGC AGC TAT GCG ATG AGC TGG GTG CGC CAA	192
Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln	
155 160 165	
GCC CCT GGG AAG GGT CTC GAG TGG GTG AGC GCG ATT AGC GGT AGC GGC	240
Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly	
170 175 180	
GGC AGC ACC TAT TAT GCG GAT AGC GTG AAA GGC CGT TTT ACC ATT TCA	288
Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser	
185 190 195 200	
CGT GAT AAT TCG AAA AAC ACC CTG TAT CTG CAA ATG AAC AGC CTG CGT	336
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg	
205 210 215	
GCG GAA GAT ACG GCC GTG TAT TAT TGC GCG CGT TGG GGC GGC GAT GGC	384
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Trp Gly Gly Asp Gly	
220 225 230	
TTT TAT GCG ATG GAT TAT TGG GGC CAA GGC ACC CTG GTG ACG GTT AGC	432
Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser	
235 240 245	
TCA GCG GGT GGC GGT TCT GGC GGC GGT GGC AGC GGT GGC GGT TCT	480
Ser Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser	

304

250	255	260	
GGC GGT GGT GGT TCC GAT ATC GTG ATG ACC CAG AGC CCA CTG AGC CTG			528
Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu			
265	270	275	280
CCA GTG ACT CCG GGC GAG CCT GCG AGC ATT AGC TGC AGA AGC AGC CAA			576
Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln			
	285	290	295
AGC CTG CTG CAT AGC AAC GGC TAT AAC TAT CTG GAT TGG TAC CTT CAA			624
Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln			
	300	305	310
AAA CCA GGT CAA AGC CCG CAG CTA TTA ATT TAT CTG GGC AGC AAC CGT			672
Lys Pro Gly Gln Ser Pro Gln Leu Ile Tyr Leu Gly Ser Asn Arg			
	315	320	325
GCC AGT GGG GTC CCG GAT CGT TTT AGC GGC TCT GGA TCC GGC ACC GAT			720
Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp			
	330	335	340
TTT ACC CTG AAA ATT AGC CGT GTG GAA GCT GAA GAC GTG GGC GTG TAT			768
Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr			
	345	350	355
TAT TGC CAG CAG CAT TAT ACC ACC CCG CCG ACC TTT GGC CAG GGT ACG			816
Tyr Cys Gln Gln His Tyr Thr Thr Pro Thr Phe Gly Gln Gly Thr			
	365	370	375
AAA GTT GAA ATT AAA CGT ACG GAA TTC			843
Lys Val Glu Ile Lys Arg Thr Glu Phe			
	380	385	

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Met	Lys	Gln	Ser	Thr	Ile	Ala	Leu	Ala	Leu	Leu	Pro	Leu	Leu	Phe	Thr
1				5					10					15	
Pro	Val	Thr	Lys	Ala	Asp	Tyr	Lys	Asp	Glu	Val	Gln	Leu	Val	Glu	Ser
			20					25					30		
Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala
		35					40					45			

Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln
 50 55 60
 Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly
 65 70 75 80
 Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 85 90 95
 Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
 100 105 110
 Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Trp Gly Gly Asp Gly
 115 120 125
 Phe Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 130 135 140
 Ser Ala Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 145 150 155 160
 Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu
 165 170 175
 Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln
 180 185 190
 Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln
 195 200 205
 Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg
 210 215 220
 Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 225 230 235 240
 Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
 245 250 255
 Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr
 260 265 270
 Lys Val Glu Ile Lys Arg Thr Glu Phe
 275 280

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

216

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Cys Ala Arg Phe Gly Lys Met Asn Tyr Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Cys Ala Arg His Arg Thr Glu Trp His Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Cys Ala Arg Val Arg Glu Leu Tyr His Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Cys Ala Arg Lys Phe Leu Lys Ala Arg Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Cys Ala Arg Trp Asn Thr Thr Gly Tyr Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Cys Ala Arg Ile Asn Glu Ala Gln Pro Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Cys Ala Arg Thr Ala Ile Thr Arg Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein .

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Cys Ala Arg Trp Tyr Asn Arg Asn Ser Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Cys Ala Arg Ser Val Gly Asp Ser Lys Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Cys Ala Arg Ser Lys Thr Phe Ala Ala Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Cys Ala Arg Val Ala Pro Gln Tyr Asp Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Cys Ala Arg Met Gln Ser Glu Trp Met Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Cys Ala Arg Tyr Phe Val His Phe Leu Tyr Thr Met Val Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Cys Ala Arg Met Ala Leu Arg Ala Ser Gly Lys Tyr Ile Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Cys Ala Arg Lys Asn Gln Met Val Phe His Ala Arg Lys Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Cys Ala Arg Thr Gln Ser Phe Trp Glu Gln Gln Lys Val Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Cys Ala Arg Tyr Pro Tyr Arg Ser Asn Phe Phe Met Pro Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3..4
- (D) OTHER INFORMATION: /product= "see Figure 10C"
/label= R*G
/note= "*" denotes codon with one-base deletion, causes
reading fr..."

shift of

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Cys Ala Arg Gly Ser Gly Ser Glu His Trp Ser Ile Phe Asp Val Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Cys Ala Arg Arg Asn Pro Trp Asn Val Asn Tyr Leu His Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Cys Ala Arg Met Lys Pro Met Leu Asn Arg Asp Gly Thr Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Cys	Ala	Arg	Lys	Gly	Ser	Glu	Phe	Leu	Glu	Thr	Asp	Val	Met	Asp	Tyr
1			5					10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Cys	Ala	Arg	Ser	Trp	Thr	Asn	Asp	Lys	Pro	Asn	Phe	Ile	Met	Asp	Val
1				5				10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Cys Ala Arg Tyr Ala Gly Thr Thr Phe Lys Gln Gly Pro Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Cys Ala Arg Lys Arg Met Met Gln Asn Pro Arg Phe Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Cys Ala Arg Arg Ser Lys Gln Lys Arg Lys Met Arg Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Cys Ala Arg Arg Asn Gly Lys Arg His Leu Arg His Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Cys Ala Arg Arg Lys Met Arg Lys Arg Ile Lys Arg Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Cys	Ala	Arg	Tyr	Arg	Lys	Ile	Met	Lys	Trp	Lys	Asn	Ser	Phe	Asp	Val
1				5				10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Cys	Ala	Arg	Leu	Ile	Glu	Val	His	Pro	Ser	Phe	Asp	Gln	Met	Asp	Val
1				5				10					15		

Trp

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

Cys Ala Arg Arg Lys Pro Met Phe Leu Lys Lys Ala Val Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Cys Ala Arg Arg Lys Phe His Arg Tyr Ser Thr Val Lys Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

Cys Ala Arg Arg Lys Thr Met Arg Ser Arg Val Lys Tyr Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 212:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

Cys Ala Arg Lys Lys Arg Ser Trp Arg Arg Met Asp Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

Cys Ala Arg Arg Asn Pro Arg Arg Gly Arg Met Asn Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Cys Ala Arg Lys Gly Lys Lys Lys Phe Ala Arg Pro Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

Cys Ala Arg Arg Met Val His Lys Gly Lys Arg Lys Ile Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Cys Ala Arg Arg Lys His Ile Thr Tyr Pro Arg Lys Gln Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

Cys Ala Arg Arg Trp Thr Lys Arg Arg Ser Phe Ala Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Cys Ala Arg Lys Lys Leu Lys Gln Tyr Thr Phe Ser Arg Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Cys Ala Arg Thr Arg Pro Trp Gln Ala Thr Arg Lys Gly Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Cys Ala Arg Asn Gln Trp Glu Phe Lys Asn Arg Arg Lys Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Cys Ala Arg Lys Arg Trp Met Trp Pro Ile Gly Lys Arg Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

Cys Ala Arg Tyr Ser Leu Trp Arg Leu Asp Glu Tyr Phe Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Cys Ala Arg Val Pro Trp Gly Asp Phe Trp Ser Trp His Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Cys Ala Arg Asn Gly Leu Glu Pro Arg His Arg Lys Met Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Cys Ala Arg Ile Met Lys Ala Pro Pro Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Cys Ala Arg Arg Lys Thr Trp His Trp Phe Tyr Lys Arg Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Cys	Ala	Arg	Trp	Lys	Asp	Met	Trp	Ser	Gln	Val	Tyr	Val	Met	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Cys	Ala	Arg	Asn	Lys	Gln	Gln	Met	Arg	Phe	Arg	Arg	Phe	Met	Asp	Tyr
1				5				10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Cys Ala Arg Asn Met Leu Ala Leu Ser Arg Gly Lys Glu Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Cys Ala Arg Asn Met Arg Leu Met Arg Met Arg Lys Asn Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Cys Ala Arg Tyr Ile Lys Gln Ala Lys Arg Lys Leu Ala Phe Asp Tyr
 1 5 10 15
 Trp

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Cys Ala Arg Tyr Asn Arg His Ala Trp Gln Lys Met Gln Phe Asp Tyr
 1 5 10 15
 Trp

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Cys Ala Arg Tyr Val Lys Tyr Ala Arg Asn Lys Met Gln Phe Asp Tyr
 1 5 10 15
 Trp

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Cys	Ala	Arg	Tyr	Lys	Arg	Gly	Ala	Trp	Met	Lys	Thr	Met	Phe	Asp	Val
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Cys	Ala	Arg	Arg	Lys	Pro	Leu	Arg	Arg	Ile	Met	Lys	Trp	Phe	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Cys Ala Arg Tyr Arg Lys Arg Ala Ser Arg Gln Met Gln Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Cys Ala Arg Gln Arg Tyr Arg Ser Lys Ile Lys Gly His Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Cys Ala Arg Trp Arg Asp Phe Asn Ser Tyr Asp Pro Met Asp Tyr Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Cys Ala Arg Met Ala Asp Leu Asp Asn Tyr Trp Val Gln Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Cys Ala Arg Leu Gln Ala Tyr Leu Lys Pro His His Trp Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Cys Ala Arg Arg Leu Ile Glu Gln Ala Arg Asp His Val Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Cys Ala Arg Ser Trp His Asn Ser Gln Phe Thr Gln Ser Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Cys Ala Arg Val Asp His Phe Gln Thr Glu Asn Glu Trp Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Cys	Ala	Arg	Asp	Trp	Pro	Thr	Leu	Ile	Phe	Trp	Tyr	Trp	Phe	Asp	Tyr
1				5					10					15	

Trp

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Cys	Ala	Arg	Gly	Phe	Gly	Phe	Thr	Glu	Asp	Tyr	Trp
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Cys Ala Arg Gln Phe Asp Glu Asp Ser Phe Val Arg Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Cys Ala Arg Ile Leu Lys Glu Ser Ser Lys Ser Arg Gln Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Cys Ala Arg Glu Gln Asp Glu Tyr Gly Ala Ile Arg Ile Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Cys Ala Arg Asn His Phe Glu Ala Ser Trp Pro Arg Arg Gln Met Asp
1 5 10 15

Val Trp

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Cys Ala Arg Glu Asn Glu Trp Val Asp Met Ile Leu Asp Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Cys Ala Arg Gln Tyr Ser Glu Thr Arg Trp Val Arg Lys Phe Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Cys Ala Arg Gln Phe Lys Glu Ser Lys Thr Arg Arg Lys Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Cys Ala Arg Lys Lys Thr Gln Tyr Val His Asp Trp Arg Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Cys Ala Arg Arg Trp Arg Glu Thr Lys Ser Lys Arg Phe Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Cys Ala Arg Asp Tyr Ile Met Glu Phe Asp Tyr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Cys Ala Arg Gln Phe Glu Glu Thr Lys Gln Arg Arg Leu Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Cys Ala Arg Asp Gln Gly Phe Tyr Ala Ile Asp Tyr Val Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Cys Ala Arg Val Phe Thr Tyr Met Tyr Asn Tyr Phe Arg Phe Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Cys Ala Arg Val Phe Phe Glu Gln Met Glu Val Val Arg Met Asp Val
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Cys Ala Arg Glu Lys Glu Tyr Arg Leu Ser Trp Ser Gln Met Asp Tyr
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Cys	Ala	Arg	Tyr	Pro	Ser	Arg	Trp	Ala	Pro	Asn	Trp	Tyr	Met	Asp	Tyr
1				5				10					15		

Trp

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Cys	Ala	Arg	Asp	Gly	Gly	Phe	Lys	Pro	Leu	Thr	His	Phe	Phe	Asp	Val
1				5				10						15	

Trp

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

ACATGTAAGC TTCCCCCCCC CCTTAATTAA CCCCCCCCCC TGTACACCCC CCCCCCGCTA 60
CCCCCCCCCC CCAGATCTCC CCCCCCCCGA CGTCCCCCCT CTAGACCCCC CCCCCGCATG 120
CCCCCCCCCC CGAATTCGAC GTC 143

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 132..989
- (D) OTHER INFORMATION: /product= "Amp resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

CAGGTGGCAC TTTTCGGGGA AATGTGCGCG GAACCCCTAT TTGTTTATTT TTCTAAATAC 60
ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCCGTGATA AATGCTTCAA TAATATTGAA 120
AAAGGAAGAG T ATG AGT ATT CAA CAT TTC CGT GTC GCC CTT ATT CCC TTT 170
Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe
285 290
TTT GCG GCA TTT TGC CTT CCT GTT TTT GCT CAC CCA GAA ACG CTG GTG 218
Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val
295 300 305 310
AAA GTA AAA GAT GCT GAA GAT CAG TTG GGT GCA CGA GTG GGT TAC ATC 266
Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile
315 320 325
GAA CTG GAT CTC AAC AGC GGT AAG ATC CTT GAG AGT TTT CGC CCC GAA 314
Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu
330 335 340
GAA CGT TTT CCA ATG ATG AGC ACT TTT AAA GTT CTG CTA TGT GGC GCG 362
Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala
345 350 355
GTA TTA TCC CGT ATT GAC GCC GGG CAA GAG CAA CTC GGT CGC CGC ATA 410

Val	Leu	Ser	Arg	Ile	Asp	Ala	Gly	Gln	Glu	Gln	Leu	Gly	Arg	Arg	Ile		
360						365					370						
CAC	TAT	TCT	CAG	AAT	GAC	TTG	GTT	GAG	TAC	TCA	CCA	GTC	ACA	GAA	AAG	458	
His	Tyr	Ser	Gln	Asn	Asp	Leu	Val	Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys		
375					380					385					390		
CAT	CTT	ACG	GAT	GGC	ATG	ACA	GTA	AGA	GAA	TTA	TGC	AGT	GCT	GCC	ATA	506	
His	Leu	Thr	Asp	Gly	Met	Thr	Val	Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile		
				395					400					405			
ACC	ATG	AGT	GAT	AAC	ACT	GCG	GCC	AAC	TTA	CTT	CTG	ACA	ACG	ATC	GGA	554	
Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly		
			410					415					420				
GGA	CCG	AAG	GAG	CTA	ACC	GCT	TTT	TTG	CAC	AAC	ATG	GGG	GAT	CAT	GTA	602	
Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	Leu	His	Asn	Met	Gly	Asp	His	Val		
		425					430					435					
ACT	CGC	CTT	GAT	CGT	TGG	GAA	CCG	GAG	CTG	AAT	GAA	GCC	ATA	CCA	AAC	650	
Thr	Arg	Leu	Asp	Arg	Trp	Glu	Pro	Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn		
	440					445					450						
GAC	GAG	CGT	GAC	ACC	ACG	ATG	CCT	GTA	GCA	ATG	GCA	ACA	ACG	TTG	CGC	698	
Asp	Glu	Arg	Asp	Thr	Thr	Met	Pro	Val	Ala	Met	Ala	Thr	Thr	Leu	Arg		
455				460						465					470		
AAA	CTA	TTA	ACT	GGC	GAA	CTA	CTT	ACT	CTA	GCT	TCC	CGG	CAA	CAA	TTA	746	
Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu		
				475				480						485			
ATA	GAC	TGG	ATG	GAG	GCG	GAT	AAA	GTT	GCA	GGA	CCA	CTT	CTG	CGC	TCG	794	
Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser		
		490					495						500				
GCC	CTT	CCG	GCT	GGC	TGG	TTT	ATT	GCT	GAT	AAA	TCT	GGA	GCC	GGT	GAG	842	
Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu		
		505				510						515					
CGT	GGG	TCT	CGC	GGT	ATC	ATT	GCA	GCA	CTG	GGG	CCA	GAT	GGT	AAG	CCC	890	
Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro		
	520				525						530						
TCC	CGT	ATC	GTA	GTT	ATC	TAC	ACG	ACG	GGG	AGT	CAG	GCA	ACT	ATG	GAT	938	
Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp		
535					540				545					550			
GAA	CGA	AAT	AGA	CAG	ATC	GCT	GAG	ATA	GGT	GCC	TCA	CTG	ATT	AAG	CAT	986	
Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	Ile	Gly	Ala	Ser	Leu	Ile	Lys	His		
			555				560						565				
TGG	TA	ACTG	TCAG	ACCA	AGTTTA	CTCATATATA	CTTTAGATTG	ATTTAAAACT								1039	
Trp																	

TCATTTTAA TTTAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAT 1099
 CCCTTAACGT GAGTTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC 1159
 TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAAA AACCACCGCT 1219
 ACCAGCGGTG GTTTGTTTGC CGGATCAAGA GCTACCAACT CTTTTTCCGA AGGTAAGTGG 1279
 CTTCAGCAGA GCGCAGATAC CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA 1339
 CTTCAAGAAC TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC 1399
 TGCTGCCAGT GCGGATAAGT CGTGTCTTAC CGGTTTGAC TCAAGACGAT AGTTACCGGA 1459
 TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA CAGCCCAGCT TGGAGCGAAC 1519
 GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCTATGA GAAAGCGCCA CGCTTCCCGA 1579
 AGGGAGAAAG GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG 1639
 GGAGCTTCCA GGGGGAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 1699
 ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG 1759
 CAACGCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTAAGCTTC 1819
 CCCCCCCCCT TAATTAACCC CCCCCCTGT ACACCCCCC CCCGCTAGCC CCCCCCCCA 1879
 GATCTCCCCC CCCCCGACGT CCCCCCTCTA GACCCCCCCC CCGCATGCCC CCCCCCCGA 1939
 ATTCACGT 1947

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15
 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80
 Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220
 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240
 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
 275 280 285

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

GACGTCTTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC 60
 CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG 120
 ACCATGATTA CGAATTTCTA GA 142

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: /product= "gIIIp ss with myc-tag, amber codon"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

GAA TTC GAG CAG AAG CTG ATC TCT GAG GAG GAT CTG TAG GGT GGT GGC 48
 Glu Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu * Gly Gly Gly
 290 295 300

TCT GGT TCC GGT GAT TTT GAT TAT GAA AAG ATG GCA AAC GCT AAT AAG 96
 Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys
 305 310 315

GGG GCT ATG ACC GAA AAT GCC GAT GAA AAC GCG CTA CAG TCT GAC GCT 144
 Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala
 320 325 330

AAA GGC AAA CTT GAT TCT GTC GCT ACT GAT TAC GGT GCT GCT ATC GAT 192
 Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp
 335 340 345 350

GGT TTC ATT GGT GAC GTT TCC GGC CTT GCT AAT GGT AAT GGT GCT ACT 240
 Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr
 355 360 365

GGT GAT TTT GCT GGC TCT AAT TCC CAA ATG GCT CAA GTC GGT GAC GGT 288
 Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly
 370 375 380

GAT AAT TCA CCT TTA ATG AAT AAT TTC CGT CAA TAT TTA CCT TCC CTC 336
 Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu

385		390		395	
CCT CAA TCG GTT GAA TGT CGC CCT TTT GTC TTT GGC GCT GGT AAA CCA	384				
Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro					
400 405 410					
TAT GAA TTT TCT ATT GAT TGT GAC AAA ATA AAC TTA TTC CGT GGT GTC	432				
Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val					
415 420 425 430					
TTT GCG TTT CTT TTA TAT GTT GCC ACC TTT ATG TAT GTA TTT TCT ACG	480				
Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr					
435 440 445					
TTT GCT AAC ATA CTG CGT AAT AAG GAG TCT TGATAAGCTT	520				
Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser					
450 455					

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Glu Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

GGGGGGGGG AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG ACATTTTTTT 60
 TGTCTGCCGT TTAATTAAAG GGGGGGGGGG GCCGGCCTGG GGGGGGGTGT ACAGGGGGGG 120
 GGG 123

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```
GCTAGCACGC GCCCTGTAGC GCGCGATTAA GCGCGGCGGG TGTGGTGGTT ACGCGCAGCG 60
TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT CGCTTCTTTC CCTTCCTTTC 120
TCGCCACGTT CGCCGGCTTT CCCCCTCAAG CTCTAAATCG GGGCATCCCT TTAGGGTTCC 180
GATTTAGTGC TTTACGGCAC CTCGACCCCA AAAAAGTTGA TTAGGGTGAT GGTTCCTGTA 240
GTGGGCCATC GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGAGTCC ACGTTCTTTA 300
ATAGTGGACT CTGTGTTCAA ACTGGAACAA CACTCAACCC TATCTCGGTC TATTCTTTTG 360
ATTTATAAGG GATTTTGCCG ATTTCCGCCT ATTGGTTAAA AAATGAGCTG ATTTAACAAA 420
AATTTAACGC GAATTTTAAC AAAATATTAA CGTTTACAAT TTCATGTACA 470
```

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 733 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```
AGATCTGACC AAAATCCCTT AACGTGAGTT TTCGTTCCAC TGAGCGTCAG ACCCCGTAGA 60
AAAGATCAAA GGATCTTCTT GAGATCCTTT TTTCTGCGC GTAATCTGCT GCTTGCAAAC 120
AAAAAACCAC CCGCTACCAG CGGTGGTTTG TTTGCCGAT CAAGAGCTAC CAACTCTTTT 180
TCCGAAGGTA ACTGGCTACA GCAGAGCGCA GATACCAAAT ACTGTTCTTC TAGTGTAGCC 240
GTAGTTAGGC CACCACTTCA AGAACTCTGT AGCACCGCCT ACATACCTCG CTCTGCTAAT 300
```

CCTGTTACCA GTGGCTGCTG CCAGTGGCGA TAAGTCGTGT CTTACCGGGT TGGACTCAAG 360
 ACGATAGTTA CCGGATAAGG CGCAGCGGTC GGGCTGAACG GGGGGTTCGT GCACACAGCC 420
 CAGCTTGGAG CGAACGACCT ACACCGAACT GAGATACCTA CAGCGTGAGC TATGAGAAAG 480
 CGCCACGCTT CCCGAAGGGA GAAAGGCGGA CAGGTATCCG GTAAGCGGCA GGGTCGGAAC 540
 AGGAGAGCGC ACGAGGGAGC TTCCAGGGGG AAACGCCTGG TATCTTTATA GTCCTGTCGG 600
 GTTTCGCCAC CTCTGACTTG AGCGTCGATT TTTGTGATGC TCGTCAGGGG GGCGGAGCCT 660
 ATGGAAAAAC GCCAGCAACG CGGCCTTTTT ACGGTTCTCT GCCTTTTGCT GGCCTTTTGC 720
 TCACATGGCT AGC 733

(2) INFORMATION FOR SEQ ID NO: 272:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic gene cassette"

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 102..758
 (D) OTHER INFORMATION: /product= "cat resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

GGGACGTCGG GTGAGGTTC AACTTTCACC ATAATGAAAT AAGATCACTA CCGGGCGTAT 60
 TTTTGTAGTT ATCGAGATTT TCAGGAGCTA AGGAAGCTAA A ATG GAG AAA AAA 113
 Met Glu Lys Lys
 ATC ACT GGA TAT ACC ACC GTT GAT ATA TCC CAA TGG CAT CGT AAA GAA 161
 Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp His Arg Lys Glu
 175 180 185 190
 CAT TTT GAG GCA TTT CAG TCA GTT GCT CAA TGT ACC TAT AAC CAG ACC 209
 His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr Tyr Asn Gln Thr
 195 200 205
 GTT CAG CTG GAT ATT ACG GCC TTT TTA AAG ACC GTA AAG AAA AAT AAG 257
 Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val Lys Lys Asn Lys
 210 215 220
 CAC AAG TTT TAT CCG GCC TTT ATT CAC ATT CTT GCC CGC CTG ATG AAT 305

His	Lys	Phe	Tyr	Pro	Ala	Phe	Ile	His	Ile	Leu	Ala	Arg	Leu	Met	Asn	
		225					230					235				
GCT	CAC	CCG	GAG	TTC	CGT	ATG	GCA	ATG	AAA	GAC	GGT	GAG	CTG	GTG	ATA	353
Ala	His	Pro	Glu	Phe	Arg	Met	Ala	Met	Lys	Asp	Gly	Glu	Leu	Val	Ile	
		240				245					250					
TGG	GAT	AGT	GTT	CAC	CCT	TGT	TAC	ACC	GTT	TTC	CAT	GAG	CAA	ACT	GAA	401
Trp	Asp	Ser	Val	His	Pro	Cys	Tyr	Thr	Val	Phe	His	Glu	Gln	Thr	Glu	
255					260					265					270	
ACG	TTT	TCA	TCG	CTC	TGG	AGT	GAA	TAC	CAC	GAC	GAT	TTC	CGG	CAG	TTT	449
Thr	Phe	Ser	Ser	Leu	Trp	Ser	Glu	Tyr	His	Asp	Asp	Phe	Arg	Gln	Phe	
				275					280					285		
CTA	CAC	ATA	TAT	TCG	CAA	GAT	GTG	GCG	TGT	TAC	GGT	GAA	AAC	CTG	GCC	497
Leu	His	Ile	Tyr	Ser	Gln	Asp	Val	Ala	Cys	Tyr	Gly	Glu	Asn	Leu	Ala	
			290					295					300			
TAT	TTC	CCT	AAA	GGG	TTT	ATT	GAG	AAT	ATG	TTT	TTC	GTC	TCA	GCC	AAT	545
Tyr	Phe	Pro	Lys	Gly	Phe	Ile	Glu	Asn	Met	Phe	Phe	Val	Ser	Ala	Asn	
		305					310					315				
CCC	TGG	GTG	AGT	TTC	ACC	AGT	TTT	GAT	TTA	AAC	GTA	GCC	AAT	ATG	GAC	593
Pro	Trp	Val	Ser	Phe	Thr	Ser	Phe	Asp	Leu	Asn	Val	Ala	Asn	Met	Asp	
		320				325					330					
AAC	TTC	TTC	GCC	CCC	GTT	TTC	ACT	ATG	GGC	AAA	TAT	TAT	ACG	CAA	GGC	641
Asn	Phe	Phe	Ala	Pro	Val	Phe	Thr	Met	Gly	Lys	Tyr	Tyr	Thr	Gln	Gly	
335				340					345						350	
GAC	AAG	GTG	CTG	ATG	CCG	CTG	GCG	ATT	CAG	GTT	CAT	CAT	GCC	GTT	TGT	689
Asp	Lys	Val	Leu	Met	Pro	Leu	Ala	Ile	Gln	Val	His	His	Ala	Val	Cys	
				355				360						365		
GAT	GGC	TTC	CAT	GTC	GGC	AGA	ATG	CTT	AAT	GAA	TTA	CAA	CAG	TAC	TGC	737
Asp	Gly	Phe	His	Val	Gly	Arg	Met	Leu	Asn	Glu	Leu	Gln	Gln	Tyr	Cys	
			370				375					380				
GAT	GAG	TGG	CAG	GGC	GGG	GCG	TAATTTTTTT	AAGGCAGTTA	TTGGGTGCCC							788
Asp	Glu	Trp	Gln	Gly	Gly	Ala										
		385														
TTAAACGCCT	GGTGCTAGAT	CTTCC														813

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp
 1 5 10 15
 His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr
 20 25 30
 Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val
 35 40 45
 Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala
 50 55 60
 Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met Lys Asp Gly
 65 70 75 80
 Glu Leu Val Ile Trp Asp Ser Val His Pro Cys Tyr Thr Val Phe His
 85 90 95
 Glu Gln Thr Glu Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp Asp
 100 105 110
 Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly
 115 120 125
 Glu Asn Leu Ala Tyr Phe Pro Lys Gly Phe Ile Glu Asn Met Phe Phe
 130 135 140
 Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val
 145 150 155 160
 Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr
 165 170 175
 Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His
 180 185 190
 His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu
 195 200 205
 Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala
 210 215

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2755 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION:3..509
 (D) OTHER INFORMATION:/product= "gIIp ss, myc tag, amber codon"

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION:complement (1853..2509)
 (D) OTHER INFORMATION:/product= "cat resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

AA	TTC	GAG	CAG	AAG	CTG	ATC	TCT	GAG	GAG	GAT	CTG	TAG	GGT	GGT	GGC	47
	Phe	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	*	Gly	Gly	Gly	
	220				225						230					
TCT	GGT	TCC	GGT	GAT	TTT	GAT	TAT	GAA	AAG	ATG	GCA	AAC	GCT	AAT	AAG	95
Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Lys	Met	Ala	Asn	Ala	Asn	Lys	
235					240					245					250	
GGG	GCT	ATG	ACC	GAA	AAT	GCC	GAT	GAA	AAC	GCG	CTA	CAG	TCT	GAC	GCT	143
Gly	Ala	Met	Thr	Glu	Asn	Ala	Asp	Glu	Asn	Ala	Leu	Gln	Ser	Asp	Ala	
				255					260					265		
AAA	GGC	AAA	CTT	GAT	TCT	GTC	GCT	ACT	GAT	TAC	GGT	GCT	GCT	ATC	GAT	191
Lys	Gly	Lys	Leu	Asp	Ser	Val	Ala	Thr	Asp	Tyr	Gly	Ala	Ala	Ile	Asp	
			270					275						280		
GGT	TTC	ATT	GGT	GAC	GTT	TCC	GGC	CTT	GCT	AAT	GGT	AAT	GGT	GCT	ACT	239
Gly	Phe	Ile	Gly	Asp	Val	Ser	Gly	Leu	Ala	Asn	Gly	Asn	Gly	Ala	Thr	
		285					290					295				
GGT	GAT	TTT	GCT	GGC	TCT	AAT	TCC	CAA	ATG	GCT	CAA	GTC	GGT	GAC	GGT	287
Gly	Asp	Phe	Ala	Gly	Ser	Asn	Ser	Gln	Met	Ala	Gln	Val	Gly	Asp	Gly	
	300					305					310					
GAT	AAT	TCA	CCT	TTA	ATG	AAT	AAT	TTC	CGT	CAA	TAT	TTA	CCT	TCC	CTC	335
Asp	Asn	Ser	Pro	Leu	Met	Asn	Asn	Phe	Arg	Gln	Tyr	Leu	Pro	Ser	Leu	
315					320				325						330	
CCT	CAA	TCG	GTT	GAA	TGT	CGC	CCT	TTT	GTC	TTT	GGC	GCT	GGT	AAA	CCA	383
Pro	Gln	Ser	Val	Glu	Cys	Arg	Pro	Phe	Val	Phe	Gly	Ala	Gly	Lys	Pro	
				335					340					345		
TAT	GAA	TTT	TCT	ATT	GAT	TGT	GAC	AAA	ATA	AAC	TTA	TTC	CGT	GGT	GTC	431
Tyr	Glu	Phe	Ser	Ile	Asp	Cys	Asp	Lys	Ile	Asn	Leu	Phe	Arg	Gly	Val	
		350						355					360			
TTT	GCG	TTT	CTT	TTA	TAT	GTT	GCC	ACC	TTT	ATG	TAT	GTA	TTT	TCT	ACG	479
Phe	Ala	Phe	Leu	Leu	Tyr	Val	Ala	Thr	Phe	Met	Tyr	Val	Phe	Ser	Thr	
		365					370					375				
TTT	GCT	AAC	ATA	CTG	CGT	AAT	AAG	GAG	TCT	TGATAAGCTT	GACCTGTGAA					529
Phe	Ala	Asn	Ile	Leu	Arg	Asn	Lys	Glu	Ser							

380

385

GTGAAAAATG GCGCAGATTG TGCACATTT TTTTGTCTG CCGTTTAATT AAAGGGGGGG	589
GGGGGCCGGC CTGGGGGGGG GTGTACATGA AATTGTAAAC GTTAATATTT TGTTAAAATT	649
CGCGTTAAAT TTTTGTAAA TCAGTCATT TTTAACCAG TAGGCCGAAA TCGGCAAAAT	709
CCCTTATAAA TCAAAGAAT AGACCGAGAT AGGGTTGAGT GTTGTTCAG TTTGGAACAA	769
GAGTCCACTA TTAAAGAACG TGGACTCCAA CGTCAAAGGG CGAAAAACCG TCTATCAGGG	829
CGATGGCCCA CTACGAGAAC CATCACCTA ATCAAGTTTT TTGGGGTCGA GGTGCCGTAA	889
AGCACTAAAT CGGAACCCTA AAGGGAGCCC CCGATTTAGA GCTTGACGGG GAAAGCCGGC	949
GAACGTGGCG AGAAAGGAAG GGAAGAAAGC GAAAGGAGCG GGCGCTAGGG CGCTGGCAAG	1009
TGTAGCGGTC ACGCTGCGCG TAACCACCAC ACCCGCCGCG CTTAATGCGC CGCTACAGGG	1069
CGCGTGCTAG CCATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA AAAGGCCGCG	1129
TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAAAAA TCGACGCTCA	1189
AGTCAGAGGT GCGGAAACCC GACAGGACTA TAAAGATACC AGGCGTTTCC CCCTGGAAGC	1249
TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC CGCCTTTCTC	1309
CCTTCGGGAA GCGTGGCGCT TTCTCATAGC TCACGCTGTA GGTATCTCAG TTCGGTGTAG	1369
GTCGTTGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA CCGCTGCGCC	1429
TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGGTAAGAC ACGACTTATC GCCACTGGCA	1489
GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC AGAGTTCTTG	1549
AAGTGGTGGC CTAACACGG CTACACTAGA AGAACAGTAT TTGGTATCTG CGCTCTGCTG	1609
TAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA AACCACCGCT	1669
GGTAGCGGTG GTTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA AGGATCTCAA	1729
GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA CTCACGTAA	1789
GGGATTTTGG TCAGATCTAG CACCAGGCGT TTAAGGGCAC CAATAACTGC CTTAAAAAAA	1849
TTACGCCCCG CCCTGCCACT CATCGCAGTA CTGTTGTAAT TCATTAAGCA TTCTGCCGAC	1909
ATGGAAGCCA TCACAAACGG CATGATGAAC CTGAATCGCC AGCGGCATCA GCACCTTGTC	1969
GCCTTGCGTA TAATATTTGC CCATAGTGAA AACGGGGGCG AAGAAGTTGT CCATATTGGC	2029
TACGTTTAAA TCAAACCTGG TGAACTCAC CCAGGGATTG GCTGAGACGA AAAACATATT	2089
CTCAATAAAC CCTTTAGGGA AATAGGCCAG GTTTTCACCG TAACACGCCA CATCTTGCGA	2149

ATATATGTGT AGAAACTGCC GGAAATCGTC GTGGTATTCA CTCCAGAGCG ATGAAAACGT 2209
 TTCAGTTTGC TCATGGAAAA CGGTGTAACA AGGGTGAACA CTATCCCATA TCACCAGCTC 2269
 ACCGTCTTTC ATTGCCATAC GGAATCCGG GTGAGCATTC ATCAGGCGGG CAAGAATGTG 2329
 AATAAAGGCC GGATAAACT TGTGCTTATT TTTCTTTACG GTCTTTAAAA AGGCCGTAAT 2389
 ATCCAGCTGA ACGGTCTGGT TATAGGTACA TTGAGCAACT GACTGAAATG CCTCAAATG 2449
 TTCTTTACGA TGCCATTGGG ATATATCAAC GGTGGTATAT CCAGTGATTT TTTTCTCCAT 2509
 TTTAGCTTCC TTAGCTCCTG AAAATCTCGA TAACTCAAAA AATACGCCCG GTAGTGATCT 2569
 TATTTTATTA TGGTGAAAGT TGGAACCTCA CCCGACGTCT AATGTGAGTT AGCTCACTCA 2629
 TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG 2689
 CGGATAACAA TTTCACACAG GAAACAGCTA TGACCATGAT TACGAATTTC TAGAGCATGC 2749
 GGGGGG 2755

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu

(2) INFORMATION FOR SEQ ID NO: 276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

Met Glu Lys Lys Ile Thr Gly Tyr Thr Val Asp Ile Ser Gln Trp
 1 5 10 15
 His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr
 20 25 30
 Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val
 35 40 45

Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala
 50 55 60
 Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met Lys Asp Gly
 65 70 75 80
 Glu Leu Val Ile Trp Asp Ser Val His Pro Cys Tyr Thr Val Phe His
 85 90 95
 Glu Gln Thr Glu Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp Asp
 100 105 110
 Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly
 115 120 125
 Glu Asn Leu Ala Tyr Phe Pro Lys Gly Phe Ile Glu Asn Met Phe Phe
 130 135 140
 Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val
 145 150 155 160
 Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr
 165 170 175
 Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His
 180 185 190
 His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu
 195 200 205
 Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala
 210 215

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GACGCTCTTAA TGTGAGTTAG CTCACCTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC 60
 CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG 120
 ACCATGTCTA GAATAACTTC GTATAATGTA CGCTATACGA AGTTATCGCA TGC 173

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TGACGTC

47

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic gene cassette"

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1245
(D) OTHER INFORMATION: /product= "gIIIp, GGGGS linker"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

GAA TTC GGT GGT GGT GGA TCT GCG TGC GCT GAA ACG GTT GAA AGT TGT	48
Glu Phe Gly Gly Gly Gly Ser Ala Cys Ala Glu Thr Val Glu Ser Cys	
220 225 230 235	
TTA GCA AAA TCC CAT ACA GAA AAT TCA TTT ACT AAC GTC TGG AAA GAC	96
Leu Ala Lys Ser His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys Asp	
240 245 250	
GAC AAA ACT TTA GAT CGT TAC GCT AAC TAT GAG GGC TGT CTG TGG AAT	144
Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp Asn	
255 260 265	
GCT ACA GGC GTT GTA GTT TGT ACT GGT GAC GAA ACT CAG TGT TAC GGT	192
Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr Gly	
270 275 280	
ACA TGG GTT CCT ATT GGG CTT GCT ATC CCT GAA AAT GAG GGT GGT GGC	240

Thr	Trp	Val	Pro	Ile	Gly	Leu	Ala	Ile	Pro	Glu	Asn	Glu	Gly	Gly	Gly		
285						290					295						
TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGT	ACT	288	
Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Thr	315	
300					305					310							
AAA	CCT	CCT	GAG	TAC	GGT	GAT	ACA	CCT	ATT	CCG	GGC	TAT	ACT	TAT	ATC	336	
Lys	Pro	Pro	Glu	Tyr	Gly	Asp	Thr	Pro	Ile	Pro	Gly	Tyr	Thr	Tyr	Ile	330	
				320					325								
AAC	CCT	CTC	GAC	GGC	ACT	TAT	CCG	CCT	GGT	ACT	GAG	CAA	AAC	CCC	GCT	384	
Asn	Pro	Leu	Asp	Gly	Thr	Tyr	Pro	Pro	Gly	Thr	Glu	Gln	Asn	Pro	Ala		
			335					340					345				
AAT	CCT	AAT	CCT	TCT	CTT	GAG	GAG	TCT	CAG	CCT	CTT	AAT	ACT	TTC	ATG	432	
Asn	Pro	Asn	Pro	Ser	Leu	Glu	Glu	Ser	Gln	Pro	Leu	Asn	Thr	Phe	Met		
			350				355					360					
TTT	CAG	AAT	AAT	AGG	TTC	CGA	AAT	AGG	CAG	GGG	GCA	TTA	ACT	GTT	TAT	480	
Phe	Gln	Asn	Asn	Arg	Phe	Arg	Asn	Arg	Gln	Gly	Ala	Leu	Thr	Val	Tyr		
	365					370					375						
ACG	GGC	ACT	GTT	ACT	CAA	GGC	ACT	GAC	CCC	GTT	AAA	ACT	TAT	TAC	CAG	528	
Thr	Gly	Thr	Val	Thr	Gln	Gly	Thr	Asp	Pro	Val	Lys	Thr	Tyr	Tyr	Gln		
380					385					390					395		
TAC	ACT	CCT	GTA	TCA	TCA	AAA	GCC	ATG	TAT	GAC	GCT	TAC	TGG	AAC	GGT	576	
Tyr	Thr	Pro	Val	Ser	Ser	Lys	Ala	Met	Tyr	Asp	Ala	Tyr	Trp	Asn	Gly		
				400					405					410			
AAA	TTC	AGA	GAC	TGC	GCT	TTC	CAT	TCT	GGC	TTT	AAT	GAG	GAT	TTA	TTT	624	
Lys	Phe	Arg	Asp	Cys	Ala	Phe	His	Ser	Gly	Phe	Asn	Glu	Asp	Leu	Phe		
			415					420				425					
GTT	TGT	GAA	TAT	CAA	GGC	CAA	TCG	TCT	GAC	CTG	CCT	CAA	CCT	CCT	GTC	672	
Val	Cys	Glu	Tyr	Gln	Gly	Gln	Ser	Ser	Asp	Leu	Pro	Gln	Pro	Pro	Val		
			430				435					440					
AAT	GCT	GGC	GGC	GGC	TCT	GGT	GGT	GGT	TCT	GGT	GGC	GGC	TCT	GAG	GGT	720	
Asn	Ala	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Gly		
	445					450					455						
GGT	GGC	TCT	GAG	GGT	GGC	GGT	TCT	GAG	GGT	GGC	GGC	TCT	GAG	GGA	GGC	768	
Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly	Gly	Ser	Glu	Gly	Gly		
460					465					470					475		
GGT	TCC	GGT	GGT	GGC	TCT	GGT	TCC	GGT	GAT	TTT	GAT	TAT	GAA	AAG	ATG	816	
Gly	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gly	Asp	Phe	Asp	Tyr	Glu	Lys	Met		
				480					485					490			
GCA	AAC	GCT	AAT	AAG	GGG	GCT	ATG	ACC	GAA	AAT	GCC	GAT	GAA	AAC	GCG	864	
Ala	Asn	Ala	Asn	Lys	Gly	Ala	Met	Thr	Glu	Asn	Ala	Asp	Glu	Asn	Ala		
			495					500					505				

356

CTA CAG TCT GAC GCT AAA GGC AAA CTT GAT TCT GTC GCT ACT GAT TAC	912
Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr	
510 515 520	
GGT GCT GCT ATC GAT GGT TTC ATT GGT GAC GTT TCC GGC CTT GCT AAT	960
Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn	
525 530 535	
GGT AAT GGT GCT ACT GGT GAT TTT GCT GGC TCT AAT TCC CAA ATG GCT	1008
Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala	
540 545 550 555	
CAA GTC GGT GAA GGT GAT AAT TCA CCT TTA ATG AAT AAT TTC CGT CAA	1056
Gln Val Gly Glu Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln	
560 565 570	
TAT TTA CCT TCC ATC CCT CAA TCG GTT GAA TGT CGC CCT TTT GTC TTT	1104
Tyr Leu Pro Ser Ile Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe	
575 580 585	
GGC GCT GGT AAA CCC TAT GAA TTT TCT ATT GAT TGT GAC AAA ATA AAC	1152
Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn	
590 595 600	
TTA TTC CGT GGT GTC TTT GCG TTT CTT TTA TAT GTT GCC ACC TTT ATG	1200
Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met	
605 610 615	
TAT GTA TTT TCT ACG TTT GCT AAC ATA CTG CGT AAT AAG GAG TCT	1245
Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser	
620 625 630	
TGATAAGCTT	1255

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

Glu Phe Gly Gly Gly Gly Ser Ala Cys Ala Glu Thr Val Glu Ser Cys	
1 5 10 15	
Leu Ala Lys Ser His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys Asp	
20 25 30	
Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp Asn	
35 40 45	

Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr Gly
 50 55 60
 Thr Trp Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu Gly Gly Gly
 65 70 75 80
 Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Thr
 85 90 95
 Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr Ile
 100 105 110
 Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala
 115 120 125
 Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met
 130 135 140
 Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr
 145 150 155 160
 Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln
 165 170 175
 Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly
 180 185 190
 Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Leu Phe
 195 200 205
 Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val
 210 215 220
 Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly
 225 230 235 240
 Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly
 245 250 255
 Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met
 260 265 270
 Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala
 275 280 285
 Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr
 290 295 300
 Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn
 305 310 315 320
 Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala
 325 330 335
 Gln Val Gly Glu Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln

Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met	
495 500 505 510	
AAT AAT TTC CGT CAA TAT TTA CCT TCC CTC CCT CAA TCG GTT GAA TGT	336
Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys	
515 520 525	
CGC CCT TTT GTC TTT GGC GCT GGT AAA CCA TAT GAA TTT TCT ATT GAT	384
Arg Pro Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp	
530 535 540	
TGT GAC AAA ATA AAC TTA TTC CGT GGT GTC TTT GCG TTT CTT TTA TAT	432
Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr	
545 550 555	
GTT GCC ACC TTT ATG TAT GTA TTT TCT ACG TTT GCT AAC ATA CTG CGT	480
Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg	
560 565 570	
AAT AAG GAG TCT TGATAAGCTT	502
Asn Lys Glu Ser	575

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

Glu Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp	
1 5 10 15	
Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala	
20 25 30	
Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val	
35 40 45	
Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser	
50 55 60	
Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn	
65 70 75 80	
Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn	
85 90 95	
Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg	
100 105 110	

200

Pro Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys
115 120 125
Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val
130 135 140
Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn
145 150 155 160
Lys Glu Ser

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

GCATGCCATA ACTTCGTATA ATGTACGCTA TACGAAGTTA TAAGCTT

47

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 82..978
(D) OTHER INFORMATION: /product= "bla resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

GGGGGTGTAC ATTCAAATAT GTATCCGCTC ATGAGACAAT AACCTGATA AATGCTTCAA 60

TAATATTGAA AAAGGAAGAG T ATG AGT ATT CAA CAT TTC CGT GTC GCC CTT 111
Met Ser Ile Gln His Phe Arg Val Ala Leu
165 170

ATT CCC TTT TTT GCG GCA TTT TGC CTT CCT GTT TTT GCT CAC CCA GAA	159
Ile Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu	
175 180 185	
ACG CTG GTG AAA GTA AAA GAT GCT GAG GAT CAG TTG GGT GCG CGA GTG	207
Thr Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val	
190 195 200 205	
GGT TAC ATC GAA CTG GAT CTC AAC AGC GGT AAG ATC CTT GAG AGT TTT	255
Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe	
210 215 220	
CGC CCC GAA GAA CGT TTT CCA ATG ATG AGC ACT TTT AAA GTT CTG CTA	303
Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu	
225 230 235	
TGT GGC GCG GTA TTA TCC CGT ATT GAC GCC GGG CAA GAG CAA CTC GGT	351
Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly	
240 245 250	
CGC CGC ATA CAC TAT TCT CAG AAT GAC TTG GTT GAG TAC TCA CCA GTC	399
Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val	
255 260 265	
ACA GAA AAG CAT CTT ACG GAT GGC ATG ACA GTA AGA GAA TTA TGC AGT	447
Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser	
270 275 280 285	
GCT GCC ATA ACC ATG AGT GAT AAC ACT GCG GCC AAC TTA CTT CTG ACA	495
Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr	
290 295 300	
ACG ATC GGA GGA CCG AAG GAG CTA ACC GCT TTT TTG CAC AAC ATG GGG	543
Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly	
305 310 315	
GAT CAT GTA ACT CGC CTT GAT CGT TGG GAA CCG GAG CTG AAT GAA GCC	591
Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala	
320 325 330	
ATA CCA AAC GAC GAG CGT GAC ACC ACG ATG CCT GTA GCA ATG GCA ACA	639
Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala Met Ala Thr	
335 340 345	
ACG TTG CGC AAA CTA TTA ACT GGC GAA CTA CTT ACT CTA GCT TCC CGG	687
Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg	
350 355 360 365	
CAA CAG TTA ATA GAC TGG ATG GAG GCG GAT AAA GTT GCA GGA CCA CTT	735
Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu	
370 375 380	
CTG CGC TCG GCC CTT CCG GCT GGC TGG TTT ATT GCT GAT AAA TCT GGA	783
Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly	
385 390 395	

GCC GGT GAG CGT GGG TCT CGC GGT ATC ATT GCA GCA CTG GGG CCA GAT 831
 Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp
 400 405 410

GGT AAG CCC TCC CGT ATC GTA GTT ATC TAC ACG ACG GGG AGT CAG GCA 879
 Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala
 415 420 425

ACT ATG GAT GAA CGA AAT AGA CAG ATC GCT GAG ATA GGT GCC TCA CTG 927
 Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu
 430 435 440 445

ATT AAG CAT TGG GTA ACT GTC AGA CCA AGT TTA CTC ATA TAT ACT TTA 975
 Ile Lys His Trp Val Thr Val Arg Pro Ser Leu Leu Ile Tyr Thr Leu
 450 455 460

GAT TGATTTAAAA CTTCATTTTT AATTTAAAG GATCTAGGTG AAGATCCTTT 1028
 Asp

TTGATAATCT CATGACCAAA ATCCCTTAAC GTGAGTTTTT GTTCCACTGA GCGTCAGACC 1088

CCGTAGAAAA GATCAAAGGA TCTTCTTGAG ATCCTTTTTG ATAATGGCCG GCCCCCCCCC 1148

TTAATTAAGG GGGGG 1163

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220
 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240
 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Val Thr
 275 280 285
 Val Arg Pro Ser Leu Leu Ile Tyr Thr Leu Asp
 290 295

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

GCTAGCACGC GCCCTGTAGC GGCGCATTAA GCGCGGCGGG TGTGGTGGTT ACGCGCAGCG 60
TGACCGCTAC ACTTGCCAGC GCCCTAGCGC CCGCTCCTTT CGCTTCTTTC CCTTCCTTTC 120
TCGCCACGTT CGCCGGCTTT CCCCCTCAAG CTCTAAATCG GGGGCTCCCT TTAGGGTTCC 180
GATTTAGTGC TTTACGGCAC CTCGACCCCA AAAAAGTGA TTAGGGTGAT GGTCTCTGTA 240
GTGGGCCATC GCCCTGATAG ACGGTTTTTC GCCCTTTGAC GTTGAGTCC ACGTTCTTTA 300
ATAGTGGACT CTTGTTCCAA ACTGGAACAA CACTCAACCC TATCTCGGTC TATCTTTTTC 360
ATTTATAAGG GATTTTGCCG ATTTCCGCCT ATTGGTTAAA AAATGAGCTG ATTTAACAAA 420
AATTTAACGC GAATTTTAAC AAAATATTAA CGTTTACAAT TTCATGTACA 470

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

AGATCTAATA AGATGATCTT CTTGAGATCG TTTTGGTCTG CGCGTAATCT CTTGCTCTGA 60
AAACGAAAAA ACCGCCTTGC AGGGCGGTTT TTCGTAGGTT CTCTGAGCTA CCAACTCTTT 120
GAACCGAGGT AACTGGCTTG GAGGAGCGCA GTCATAAAA CTTGTCCTTT CAGTTTAGCC 180
TTAACCGGCG CATGACTTCA AGACTAACTC CTCTAAATCA ATTACCAGTG GCTGCTGCCA 240
GTGGTGCTTT TGCATGTCTT TCCGGGTTGG ACTCAAGACG ATAGTTACCG GATAAGGCGC 300
AGCGGTCGGA CTGAACGGGG GGTTCGTGCA TACAGTCCAG CTTGGAGCGA ACTGCCTACC 360
CGGAAGTGAG TGTCAGGCGT GGAATGAGAC AAACGCGGCC ATAACAGCGG AATGACACCG 420
GTAAACCGAA AGGCAGGAAC AGGAGAGCGC AGGAGGGAGC CGCCAGGGGG AAACGCCTGG 480
TATCTTTATA GTCCTGTCGG GTTTCGCCAC CACTGATTG AGCGTCAGAT TTCGTGATGC 540
TTGTCAGGGG GCGGAGCCT ATGGA AAAAC GGCTTTGCCG CGGCCCTCTC ACTTCCTGT 600
TAAGTATCTT CCTGGCATCT TCCAGGAAAT CTCCGCCCCG TTCGTAAGCC ATTTCCGCTC 660
GCCGCAGTCG AACGACCGAG CGTAGCGAGT CAGTGAGCGA GGAAGCGGAA TATATCCTGT 720

ATCACATATT CTGCTGACGC ACCGGTGCAG CCTTTTTTCT CCTGCCACAT GAAGCACTTC 780
 ACTGACACCC TCATCAGTGC CAACATAGTA AGCCAGTATA CACTCCGCTA GC 832

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

AGATCTCATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TTCAGATCT 49

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT GGCACCTTA 60
 CCGTTGCTCT TCACCCCTGT TACCAAAGCC GAATTC 96

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

TCTAGAGCAT GCGTAGGAGA AAATAAAATG AAACAAAGCA CTATTGCACT GGCACCTCTTA 60
CCGTTGCTCT TCACCCCTGT TACCAAAGCC GACTACAAAG ATGAAGTGCA ATTGGAATTC 120

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 96 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic DNA cassette"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

TCTAGAGGTT GAGGTGATTT TATGAAAAG AATATCGCAT TTCTTCTTGC ATCTATGTTT 60
GTTTTTCTA TTGCTACAAA TGCATACGCT GAATTC 96

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 79..1158
(D) OTHER INFORMATION: /product= "lacI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

GCTAGCATCG AATGGCGCAA AACCTTTCGC GGTATGGCAT GATAGCGCCC GGAAGAGAGT 60
CAATTCAGGG TGGTGAAT GTG AAA CCA GTA ACG TTA TAC GAT GTC GCA GAG 111
Val Lys Pro Val Thr Leu Tyr Asp Val Ala Glu
300 305 310
TAT GCC GGT GTC TCT TAT GAG ACC GTT TCC CGC GTG GTG AAC CAG GCC 159
Tyr Ala Gly Val Ser Tyr Gln Thr Val Ser Arg Val Val Asn Gln Ala

315										320					325					
AGC	CAC	GTT	TCT	GCG	AAA	ACG	CGG	GAA	AAA	GTG	GAA	GCG	GCG	ATG	GCG	207				
Ser	His	Val	Ser	Ala	Lys	Thr	Arg	Glu	Lys	Val	Glu	Ala	Ala	Met	Ala					
330										335					340					
GAG	CTG	AAT	TAC	ATT	CCT	AAC	CGC	GTG	GCA	CAA	CAA	CTG	GCG	GGC	AAA	255				
Glu	Leu	Asn	Tyr	Ile	Pro	Asn	Arg	Val	Ala	Gln	Gln	Leu	Ala	Gly	Lys					
345										350					355					
CAG	TCG	TTG	CTG	ATT	GGC	GTT	GCC	ACC	TCC	AGT	CTG	GCC	CTG	CAC	GCG	303				
Gln	Ser	Leu	Leu	Ile	Gly	Val	Ala	Thr	Ser	Ser	Leu	Ala	Leu	His	Ala					
360										365					370					
CCG	TCG	CAA	ATT	GTC	GCG	GCG	ATT	AAA	TCT	CGC	GCC	GAT	CAA	CTG	GGT	351				
Pro	Ser	Gln	Ile	Val	Ala	Ala	Ile	Lys	Ser	Arg	Ala	Asp	Gln	Leu	Gly					
375										380					385					
GCC	AGC	GTG	GTC	GTG	TCG	ATG	GTA	GAA	CGA	AGC	GGC	GTC	GAA	GCC	TGT	399				
Ala	Ser	Val	Val	Val	Ser	Met	Val	Glu	Arg	Ser	Gly	Val	Glu	Ala	Cys					
395										400					405					
AAA	GCG	GCG	GTG	CAC	AAT	CTT	CTC	GCG	CAA	CGT	GTC	AGT	GGG	CTG	ATT	447				
Lys	Ala	Ala	Val	His	Asn	Leu	Leu	Ala	Gln	Arg	Val	Ser	Gly	Leu	Ile					
410										415					420					
ATT	AAC	TAT	CCG	CTG	GAT	GAC	CAG	GAT	GCT	ATT	GCT	GTG	GAA	GCT	GCC	495				
Ile	Asn	Tyr	Pro	Leu	Asp	Asp	Gln	Asp	Ala	Ile	Ala	Val	Glu	Ala	Ala					
425										430					435					
TGC	ACT	AAT	GTT	CCG	GCG	TTA	TTT	CTT	GAT	GTC	TCT	GAC	CAG	ACA	CCC	543				
Cys	Thr	Asn	Val	Pro	Ala	Leu	Phe	Leu	Asp	Val	Ser	Asp	Gln	Thr	Pro					
440										445					450					
ATC	AAC	AGT	ATT	ATT	TTC	TCC	CAT	GAG	GAC	GGT	ACG	CGA	CTG	GGC	GTG	591				
Ile	Asn	Ser	Ile	Ile	Phe	Ser	His	Glu	Asp	Gly	Thr	Arg	Leu	Gly	Val					
455										460					465					
GAG	CAT	CTG	GTC	GCA	TTG	GGC	CAC	CAG	CAA	ATC	GCG	CTG	TTA	GCT	GGC	639				
Glu	His	Leu	Val	Ala	Leu	Gly	His	Gln	Gln	Ile	Ala	Leu	Leu	Ala	Gly					
475										480					485					
CCA	TTA	AGT	TCT	GTC	TCG	GCG	CGT	CTG	CGT	CTG	GCT	GGC	TGG	CAT	AAA	687				
Pro	Leu	Ser	Ser	Val	Ser	Ala	Arg	Leu	Arg	Leu	Ala	Gly	Trp	His	Lys					
490										495					500					
TAT	CTC	ACT	CGC	AAT	CAA	ATT	CAG	CCG	ATA	GCG	GAA	CGG	GAA	GGC	GAC	735				
Tyr	Leu	Thr	Arg	Asn	Gln	Ile	Gln	Pro	Ile	Ala	Glu	Arg	Glu	Gly	Asp					
505										510					515					
TGG	AGT	GCC	ATG	TCC	GGT	TTT	CAA	CAA	ACC	ATG	CAA	ATG	CTG	AAT	GAG	783				
Trp	Ser	Ala	Met	Ser	Gly	Phe	Gln	Gln	Thr	Met	Gln	Met	Leu	Asn	Glu					
520										525					530					

GGC ATC GTT CCC ACT GCG ATG CTG GTT GCC AAC GAT CAG ATG GCG CTG	831
Gly Ile Val Pro Thr Ala Met Leu Val Ala Asn Asp Gln Met Ala Leu	
535 540 545 550	
GGC GCA ATG CGT GCC ATT ACC GAG TCC GGG CTG CGC GTT GGT GCG GAC	879
Gly Ala Met Arg Ala Ile Thr Glu Ser Gly Leu Arg Val Gly Ala Asp	
555 560 565	
ATC TCG GTA GTG GGA TAC GAC GAT ACC GAG GAC AGC TCA TGT TAT ATC	927
Ile Ser Val Val Gly Tyr Asp Asp Thr Glu Asp Ser Ser Cys Tyr Ile	
570 575 580	
CCG CCG CTG ACC ACC ATC AAA CAG GAT TTT CGC CTG CTG GGG CAA ACC	975
Pro Pro Leu Thr Thr Ile Lys Gln Asp Phe Arg Leu Leu Gly Gln Thr	
585 590 595	
AGC GTG GAC CGC TTG CTG CAA CTC TCT CAG GGC CAG GCG GTG AAG GGC	1023
Ser Val Asp Arg Leu Leu Gln Leu Ser Gln Gly Gln Ala Val Lys Gly	
600 605 610	
AAT CAG CTG TTG CCC GTC TCA CTG GTG AAA AGA AAA ACC ACC CTG GCT	1071
Asn Gln Leu Leu Pro Val Ser Leu Val Lys Arg Lys Thr Thr Leu Ala	
615 620 625 630	
CCC AAT ACG CAA ACC GCC TCT CCC CGC GCG TTG GCC GAT TCA CTG ATG	1119
Pro Asn Thr Gln Thr Ala Ser Pro Arg Ala Leu Ala Asp Ser Leu Met	
635 640 645	
CAG CTG GCA CGA CAG GTT TCC CGA CTG GAA AGC GGG CAG TGAGGCTACC	1168
Gln Leu Ala Arg Gln Val Ser Arg Leu Glu Ser Gly Gln	
650 655	
CGATAAAAGC GGCTTCCTGA CAGGAGGCCG TTTTGTTTTG CAGCCCACTT AAG	1221

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Val Lys Pro Val Thr Leu Tyr Asp Val Ala Glu Tyr Ala Gly Val Ser	
1 5 10 15	
Tyr Gln Thr Val Ser Arg Val Val Asn Gln Ala Ser His Val Ser Ala	
20 25 30	
Lys Thr Arg Glu Lys Val Glu Ala Ala Met Ala Glu Leu Asn Tyr Ile	
35 40 45	
Pro Asn Arg Val Ala Gln Gln Leu Ala Gly Lys Gln Ser Leu Leu Ile	

50	55	60
Gly Val Ala Thr Ser Ser Leu Ala Leu His Ala Pro Ser Gln Ile Val 65 70 75 80		
Ala Ala Ile Lys Ser Arg Ala Asp Gln Leu Gly Ala Ser Val Val Val 85 90 95		
Ser Met Val Glu Arg Ser Gly Val Glu Ala Cys Lys Ala Ala Val His 100 105 110		
Asn Leu Leu Ala Gln Arg Val Ser Gly Leu Ile Ile Asn Tyr Pro Leu 115 120 125		
Asp Asp Gln Asp Ala Ile Ala Val Glu Ala Ala Cys Thr Asn Val Pro 130 135 140		
Ala Leu Phe Leu Asp Val Ser Asp Gln Thr Pro Ile Asn Ser Ile Ile 145 150 155 160		
Phe Ser His Glu Asp Gly Thr Arg Leu Gly Val Glu His Leu Val Ala 165 170 175		
Leu Gly His Gln Gln Ile Ala Leu Leu Ala Gly Pro Leu Ser Ser Val 180 185 190		
Ser Ala Arg Leu Arg Leu Ala Gly Trp His Lys Tyr Leu Thr Arg Asn 195 200 205		
Gln Ile Gln Pro Ile Ala Glu Arg Glu Gly Asp Trp Ser Ala Met Ser 210 215 220		
Gly Phe Gln Gln Thr Met Gln Met Leu Asn Glu Gly Ile Val Pro Thr 225 230 235 240		
Ala Met Leu Val Ala Asn Asp Gln Met Ala Leu Gly Ala Met Arg Ala 245 250 255		
Ile Thr Glu Ser Gly Leu Arg Val Gly Ala Asp Ile Ser Val Val Gly 260 265 270		
Tyr Asp Asp Thr Glu Asp Ser Ser Cys Tyr Ile Pro Pro Leu Thr Thr 275 280 285		
Ile Lys Gln Asp Phe Arg Leu Leu Gly Gln Thr Ser Val Asp Arg Leu 290 295 300		
Leu Gln Leu Ser Gln Gly Gln Ala Val Lys Gly Asn Gln Leu Leu Pro 305 310 315 320		
Val Ser Leu Val Lys Arg Lys Thr Thr Leu Ala Pro Asn Thr Gln Thr 325 330 335		
Ala Ser Pro Arg Ala Leu Ala Asp Ser Leu Met Gln Leu Ala Arg Gln 340 345 350		

Val Ser Arg Leu Glu Ser Gly Gln
355 360

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2380 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic vector"

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: complement (51..707)
(D) OTHER INFORMATION: /product= "cat resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

GATCTAGCAC CAGGCGTTTA AGGGCACCAA TAACTGCCTT AAAAAAATTA CGCCCCGCCC 60
TGCCACTCAT CGCAGTACTG TTGTAATTCA TTAAGCATTC TGCCGACATG GAAGCCATCA 120
CAAACGGCAT GATGAACCTG AATCGCCAGC GGCATCAGCA CCTTGTGCGC TTGCGTATAA 180
TATTTGCCCA TAGTGAAAAC GGGGGCGAAG AAGTTGTCCA TATTGGCTAC GTTTAAATCA 240
AAACTGGTGA AACTCACCCA GGGATTGGCT GAGACGAAA ACATATTCTC AATAAACCTT 300
TTAGGGAAAT AGGCCAGGTT TTCACCGTAA CAGCCACAT CTTGCGAATA TATGTGTAGA 360
AACTGCCGGA AATCGTCGTG GTATTCATC CAGAGCGATG AAAACGTTTC AGTTTGCTCA 420
TGAAAACGG TGTACAAGG GTGAACACTA TCCCATATCA CCAGCTCACC GTCTTTCATT 480
GCCATACGGA ACTCCGGGTG AGCATTCATC AGGCGGGCAA GAATGTGAAT AAAGGCCGGA 540
TAAACTTGT GCTTATTTT CTTTACGGTC TTAAAAAGG CCGTAATATC CAGCTGAACG 600
GTCTGGTTAT AGGTACATTG AGCAACTGAC TGAAATGCCT CAAATGTTC TTTACGATGC 660
CATTGGGATA TATCAACGGT GGTATATCCA GTGATTTTT TCTCCATTT AGCTTCCTTA 720
GCTCCTGAAA ATCTCGATAA CTCAAAAAT ACGCCCGGTA GTGATCTTAT TTCATTATGG 780
TGAAAGTTGG AACCTACCC GACGTCTAAT GTGAGTTAGC TCACTCATTA GGCACCCAG 840
GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT 900
CACACAGGAA ACAGCTATGA CCAATGATTAC GAATTTCTAG ACCCCCCCCC CGCATGCCAT 960

AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA CCTGTGAAGT GAAAAATGGC 1020
 GCAGATTGTG CGACATTTTT TTTGTCTGCC GTTTAATTAA AGGGGGGGGG GGGCCGGCCT 1080
 GGGGGGGGGT GTACATGAAA TTGTAAACGT TAATATTTTG TTTAAATTCG CGTTAAATTT 1140
 TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAATCC CTTATAAATC 1200
 AAAAGAATAG ACCGAGATAG GGTGAGTGT TGTTCAGTT TGAACAAGA GTCCACTATT 1260
 AAAGAACGTG GACTCCAACG TCAAAGGGCG AAAAACCGTC TATCAGGGCG ATGGCCCACT 1320
 ACGAGAACCA TCACCCTAAT CAAGTTTTTT GGGGTCGAGG TGCCGTAAAG CACTAAATCG 1380
 GAACCCTAAA GGGAGCCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG 1440
 AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG TAGCGGTCAC 1500
 GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCCG CTACAGGGCG CGTGCTAGCG 1560
 GAGTGTATAC TGGCTTACTA TGTGGCACT GATGAGGGTG TCAGTGAAGT GCTTCATGTG 1620
 GCAGGAGAAA AAAGGCTGCA CCGGTGCGTC AGCAGAATAT GTGATACAGG ATATATTCCG 1680
 CTCCTCGCT CACTGACTCG CTACGCTCGG TCGTTCGACT GCGGCGAGCG GAAATGGCTT 1740
 ACGAACGGGG CGGAGATTTC CTGGAAGATG CCAGGAAGAT ACTTAACAGG GAAGTGAGAG 1800
 GGCCGCGGCA AAGCCGTTTT TCCATAGGCT CCGCCCCCT GACAAGCATC ACGAAATCTG 1860
 ACGCTCAAAT CAGTGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC 1920
 TGGCGGCTCC CTCCTGCGCT CTCCTGTTCC TGCCTTTCGG TTTACCGGTG TCATTCCGCT 1980
 GTTATGGCCG CGTTTGTCTC ATTCCACGCC TGACACTCAG TTCCGGGTAG GCAGTTCGCT 2040
 CCAAGCTGGA CTGTATGCAC GAACCCCCC TTCAGTCCGA CCGCTGCGCC TTATCCGGTA 2100
 ACTATCGTCT TGAGTCCAAC CCGGAAAGAC ATGCAAAAGC ACCACTGGCA GCAGCCACTG 2160
 GTAATTGATT TAGAGGAGTT AGTCTTGAAG TCATGCGCCG GTTAAGGCTA AACTGAAAGG 2220
 ACAAGTTTTA GTGACTGCGC TCCTCCAAGC CAGTTACCTC GGTTCAAAGA GTTGGTAGCT 2280
 CAGAGAACCT ACGAAAAACC GCCCTGCAAG GCGGTTTTTT CGTTTTTCAGA GCAAGAGATT 2340
 ACGCGCAGAC CAAAACGATC TCAAGAAGAT CATCTTATTA 2380

(2) INFORMATION FOR SEQ ID NO: 295:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp
1 5 10 15
His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr
20 25 30
Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val
35 40 45
Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala
50 55 60
Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met Lys Asp Gly
65 70 75 80
Glu Leu Val Ile Trp Asp Ser Val His Pro Cys Tyr Thr Val Phe His
85 90 95
Glu Gln Thr Glu Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp Asp
100 105 110
Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly
115 120 125
Glu Asn Leu Ala Tyr Phe Pro Lys Gly Phe Ile Glu Asn Met Phe Phe
130 135 140
Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val
145 150 155 160
Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr
165 170 175
Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His
180 185 190
His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu
195 200 205
Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala
210 215

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3488 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: complement (1341..1997)
(D) OTHER INFORMATION: /product= "cat resistance"

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: complement (2521..3417)
(D) OTHER INFORMATION: /product= "bla resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

GTACATGAAA TTGTAAACGT TAATATTTTG TTAAATTCG CGTTAAATTT TTGTTAAATC 60
AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC CTTATAAATC AAAAGAATAG 120
ACCGAGATAG GGTGAGTGT TGTTCAGTT TGGAACAAGA GTCCACTATT AAAGAACGTG 180
GACTCCAACG TCAAAGGGCG AAAAACCGTC TATCAGGGCG ATGGCCCACT ACGAGAACCA 240
TCACCTAAT CAAGTTTTTT GGGGTCGAGG TGCCGTAAAG CACTAAATCG GAACCTAAA 300
GGGAGCCCC GATTAGAGC TTGACGGGA AAGCCGGCGA ACGTGGCGAG AAAGGAAGGG 360
AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG TAGCGGTCAC GCTGCGGTA 420
ACCACCACAC CGCCGCGCT TAATGCGCCG CTACAGGGCG CGTGCTAGCG GAGTGTATAC 480
TGGCTTACTA TGTTGGCACT GATGAGGGTG TCAAGTGAAG GCTTCATGTG GCAGGAGAAA 540
AAAGGCTGCA CCGGTGCGTC AGCAGAATAT GTGATACAGG ATATATCCG CTTCCTCGCT 600
CACTGACTCG CTACGCTCGG TCGTTCGACT GCGGCGAGCG GAAATGGCTT ACGAACGGGG 660
CGGAGATTTC CTGGAAGATG CCAGGAAGAT ACTTAACAGG GAAGTGAGAG GGCCGCGGCA 720
AAGCCGTTTT TCCATAGGCT CCGCCCCCT GACAAGCATC ACGAAATCTG ACGCTCAAAT 780
CAGTGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCC TGGCGGCTCC 840
CTCCTGCGCT CTCCTGTTCC TGCCTTTCGG TTTACCGGTG TCATTCCGCT GTTATGGCCG 900
CGTTTGTCTC ATTCCACGCC TGACACTCAG TTCCGGGTAG GCAGTTCGCT CCAAGCTGGA 960
CTGTATGCAC GAACCCCCCG TTCAGTCCGA CCGCTGCGCC TTATCCGGTA ACTATCGTCT 1020
TGAGTCCAAC CCGGAAAGAC ATGCAAAAGC ACCACTGGCA GCAGCCACTG GTAATTGATT 1080
TAGAGGAGTT AGTCTTGAAG TCATGCGCCG GTTAAGGCTA AACTGAAAGG ACAAGTTTTA 1140
GTGACTGCGC TCCTCCAAGC CAGTTACCTC GGTTCAAAGA GTTGGTAGCT CAGAGAACCT 1200
ACGAAAACC GCCCTGCAAG GCGGTTTTTT CGTTTTTACA GCAAGAGATT ACGCGCAGAC 1260

CAAAACGATC	TCAAGAAGAT	CATCTTATTA	GATCTAGCAC	CAGGCGTTTA	AGGGCACCAA	1320
TAAGTGCCTT	AAAAAATTA	CGCCCCGCC	TGCCACTCAT	CGCAGTACTG	TTGTAATTCA	1380
TTAAGCATT	TGCCGACATG	GAAGCCATCA	CAAACGGCAT	GATGAACCTG	AATCGCCAGC	1440
GGCATCAGCA	CCTTGTCGCC	TTGCGTATAA	TATTTGCCCA	TAGTGAAAAC	GGGGGCGAAG	1500
AAGTTGTCCA	TATTGGCTAC	GTTTAAATCA	AACTGGTGA	AACTCACCCA	GGGATTGGCT	1560
GAGACGAAAA	ACATATTCTC	AATAAACCTT	TTAGGGAAAT	AGGCCAGGTT	TTCACCGTAA	1620
CACGCCACAT	CTTGCGAATA	TATGTGTAGA	AACTGCCGGA	AATCGTCGTG	GTATTCACTC	1680
CAGAGCGATG	AAAACGTTTC	AGTTTGCTCA	TGAAAACGG	TGTAACAAGG	GTGAACACTA	1740
TCCCATATCA	CCAGCTCACC	GTCTTTCATT	GCCATACGGA	ACTCCGGGTG	AGCATTTCATC	1800
AGGCGGGCAA	GAATGTGAAT	AAAGGCCGGA	TAAAACTGT	GCTTATTTT	CTTTACGGTC	1860
TTTAAAAGG	CCGTAATATC	CAGCTGAACG	GTCTGGTTAT	AGGTACATTG	AGCAACTGAC	1920
TGAAATGCCT	CAAAATGTTT	TTTACGATGC	CATTGGGATA	TATCAACGGT	GGTATATCCA	1980
GTGATTTTTT	TCTCCATTTT	AGCTTCCTTA	GCTCCTGAAA	ATCTCGATAA	CTCAAAAAT	2040
ACGCCCCGTA	GTGATCTTAT	TTCATTATGG	TGAAAGTTGG	AACCTCACCC	GACGTCTAAT	2100
GTGAGTTAGC	TCATCATTAA	GGCACCCAG	GCTTTACACT	TTATGCTTCC	GGCTCGTATG	2160
TTGTGTGGAA	TTGTGAGCGG	ATAACAATTT	CACACAGGAA	ACAGCTATGA	CCATGATTAC	2220
GAATTTCTAG	ACCCCCCCCC	CGCATGCCAT	AACTTCGTAT	AATGTACGCT	ATACGAAGTT	2280
ATAAGCTTGA	CCTGTGAAGT	GAAAAATGGC	GCAGATTGTG	CGACATTTT	TTTGTCTGCC	2340
GTTTAATTAA	GGGGGGGGGC	CGGCCATTAT	CAAAAAGGAT	CTCAAGAAGA	TCCTTTGATC	2400
TTTTCTACGG	GGTCTGACGC	TCAGTGAAC	GAAAACCTAC	GTTAAGGGAT	TTTGGTCATG	2460
AGATTATCAA	AAAGGATCTT	CACCTAGATC	CTTTTAAATT	AAAAATGAAG	TTTTAAATCA	2520
ATCTAAAGTA	TATATGAGTA	AACTTGGTCT	GACAGTTACC	CAATGCTTAA	TCAGTGAGGC	2580
ACCTATCTCA	GCGATCTGTC	TATTTGTTTC	ATCCATAGTT	GCCTGACTCC	CCGTCGTGTA	2640
GATAACTACG	ATACGGGAGG	GCTTACCATC	TGGCCCCAGT	GCTGCAATGA	TACCGCGAGA	2700
CCCACGCTCA	CCGGCTCCAG	ATTTATCAGC	AATAAACCCAG	CCAGCCGGAA	GGGCCGAGCG	2760
CAGAAGTGGT	CCTGCAACTT	TATCCGCCTC	CATCCAGTCT	ATTAAGTGT	GCCGGGAAGC	2820
TAGAGTAAGT	AGTTCGCCAG	TTAATAGTTT	GCGCAACGTT	GTTGCCATTG	CTACAGGCAT	2880
CGTGGTGTCA	CGCTCGTCGT	TTGGTATGGC	TTCATTTCAGC	TCCGGTCCCC	AACGATCAAG	2940

GCGAGTTACA TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT 3000
 CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA 3060
 TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTCTGTG ACTGGTGAGT ACTCAACCAA 3120
 GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA 3180
 TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG 3240
 GCGAAAAC TC AAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGCGC 3300
 ACCCAACTGA TCCTCAGCAT CTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAAACAGG 3360
 AAGGCAAAAT GCCGCAAAA AGGGAATAAG GCGGACACGG AAATGTTGAA TACTCATACT 3420
 CTTCTTTTT CAATATTATT GAAGCATTTA TCAGGTTAT TGTCTCATGA GCGGATACAT 3480
 ATTTGAAT 3488

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Trp
 1 5 10 15
 His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr
 20 25 30
 Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val
 35 40 45
 Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala
 50 55 60
 Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met Lys Asp Gly
 65 70 75 80
 Glu Leu Val Ile Trp Asp Ser Val His Pro Cys Tyr Thr Val Phe His
 85 90 95
 Glu Gln Thr Glu Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp Asp
 100 105 110
 Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly
 115 120 125

Glu Asn Leu Ala Tyr Phe Pro Lys Gly Phe Ile Glu Asn Met Phe Phe
 130 135 140
 Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val
 145 150 155 160
 Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr
 165 170 175
 Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His
 180 185 190
 His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu
 195 200 205
 Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala
 210 215

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 299 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15
 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80
 Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220
 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240
 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Val Thr
 275 280 285
 Val Arg Pro Ser Leu Leu Ile Tyr Thr Leu Asp
 290 295

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic vector"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (471..1367)
- (D) OTHER INFORMATION: /product= "bla resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

GATCTCATAA CTTGCTATAA TGTATGCTAT ACGAAGTTAT GACGTCTAAT GTGAGTTAGC 60
 TCACTCATTA GGCACCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA 120
 TTGTGAGCGG ATAACAATTT CACACAGGAA ACAGCTATGA CCATGATTAC GAATTTCTAG 180

ACCCCCCCCC CGCATGCCAT AACTTCGTAT AATGTACGCT ATACGAAGTT ATAAGCTTGA 240
 CCTGTGAAGT GAAAAATGGC GCAGATTGTG CGACATTTTT TTTGTCTGCC GTTTAATTAA 300
 GGGGGGGGGC CGGCCATTAT CAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG 360
 GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA 420
 AAAGGATCTT CACCTAGATC CTTTTAAAT AAAAATGAAG TTTTAAATCA ATCTAAAGTA 480
 TATATGAGTA AACTTGGTCT GACAGTTACC CAATGCTTAA TCAGTGAGGC ACCTATCTCA 540
 GCGATCTGTC TATTTCTGTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA GATAACTACG 600
 ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA CCCACGCTCA 660
 CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA GGGCCGAGCG CAGAAGTGGT 720
 CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAAGTGT GCCGGGAAGC TAGAGTAAGT 780
 AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT CGTGGTGTCA 840
 CGCTCGTCGT TTGGTATGGC TTCATTACGC TCCGGTCCC AACGATCAAG GCGAGTTACA 900
 TGATCCCCCA TGTTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT CGTTGTGAGA 960
 AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA TTCTCTTACT 1020
 GTCATGCCAT CCGTAAGATG CTTTTCTGTG ACTGGTGAGT ACTCAACCAA GTCATTCTGA 1080
 GAATAGTGTA TGCGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA TAATACCGCG 1140
 CCACATAGCA GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG GCGAAAACCTC 1200
 TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGCGC ACCCAACTGA 1260
 TCCTCAGCAT CTTTTACTTT CACCAGCGTT TCTGGGTGAG CAAAACAGG AAGGCAAAAT 1320
 GCCGCAAAAA AGGGAATAAG GGCACACGG AAATGTTGAA TACTCATACT CTTCCTTTTT 1380
 CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT ATTTGAATGT 1440
 ACATGAAATT GTAAACGTTA ATATTTTGTT AAAATTCGCG TTAAATTTTT GTTAAATCAG 1500
 CTCATTTTTT AACCAATAGG CCGAAATCGG CAAAATCCCT TATAAATCAA AAGAATAGAC 1560
 CGAGATAGGG TTGAGTGTTG TTCCAGTTTG GAACAAGAGT CCACTATTAA AGAACGTGGA 1620
 CTCCAACGTC AAAGGGCGAA AAACCGTCTA TCAGGGCGAT GGCCCACTAC GAGAACCATC 1680
 ACCCTAATCA AGTTTTTTGG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG 1740
 GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA AGGAAGGGAA 1800
 GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA GCGGTCACGC TGCGCGTAAC 1860

CACCACACCC GCCGCGCTTA ATGCGCCGCT ACAGGGCGCG TGCTAGCGGA GTGTATACTG 1920
 GCTTACTATG TTGGCACTGA TGAGGGTGTC AGTGAAGTGC TTCATGTGGC AGGAGAAAAA 1980
 AGGCTGCACC GGTGCGTCAG CAGAATATGT GATACAGGAT ATATTCCGCT TCCTCGCTCA 2040
 CTGACTCGCT ACGCTCGGTC GTTCGACTGC GGCGAGCGGA AATGGCTTAC GAACGGGGCG 2100
 GAGATTTCTT GGAAGATGCC AGGAAGATAC TTAACAGGGA AGTGAGAGGG CCGCGGCAAA 2160
 GCCGTTTTTC CATAGGCTCC GCCCCCTGA CAAGCATCAC GAAATCTGAC GCTCAAATCA 2220
 GTGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GCGGCTCCCT 2280
 CCTGCGCTCT CCTGTTCTTG CCTTTCGGTT TACCGGTGTC ATTCCGCTGT TATGGCCGCG 2340
 TTTGTCTCAT TCCACGCCTG ACACTCAGTT CCGGGTAGGC AGTTCGCTCC AAGCTGGACT 2400
 GTATGCACGA ACCCCCCGTT CAGTCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG 2460
 AGTCCAACCC GGAAAGACAT GCAAAAGCAC CACTGGCAGC AGCCACTGGT AATTGATTTA 2520
 GAGGAGTTAG TCTTGAAGTC ATGCGCCGGT TAAGGCTAAA CTGAAAGGAC AAGTTTTAGT 2580
 GACTGCGCTC CTCCAAGCCA GTTACCTCGG TTCAAAGAGT TGGTAGCTCA GAGAACCTAC 2640
 GAAAAACCGC CCTGCAAGGC GGTTTTTTCG TTTTCAGAGC AAGAGATTAC GCGCAGACCA 2700
 AAACGATCTC AAGAAGATCA TCTTATTA 2728

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 299 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15
 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220
 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240
 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp Val Thr
 275 280 285
 Val Arg Pro Ser Leu Leu Ile Tyr Thr Leu Asp
 290 295

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:
TATGAGATCT CATAACTTCG TATAATGTAC GCTATACGAA GTTAT 45

(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:
TAATAACTTC GTATAGCATA CATTATACGA AGTTATGAGA TCTCA 45

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:
CATTTTTTGC CCTCGTTATC TACGCATGCG ATAACTTCGT ATAGCGTACA TTATACGAAG 60
TTATTCTAGA CATGGTCATA GCTGTTTCCT G 91

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GGGGGGAATT CGGTGGTGGT GGATCTGCGT GCGCTGAAAC GGTGAAAGT TG

52

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

CCCCCCAAG CTTATCAAGA CTCCTTATTA CG

32

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

GGGGGGGAA TTCGAGGCG GTTCCGGTGG TGCG

34

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

GGGGGGGAA TTCGAGCAGA AGCTGATCTC TGAGGAGGAT CTGTAGGGTG GTGGCTCTGG 60
TTCCGGTGAT TTTG 74

(2) INFORMATION FOR SEQ ID NO: 308:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

CCATAACTTC GTATAATGTA CGCTATACGA AGTTATA 37

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

AGCTTATAAC TTCGTATAGC GTACATTATA CGAAGTTATG GCATG 45

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AGCTTGACCT GTGAAGTGAA AAATGGCGCA GATTGTGCGA CATTTTTTTT GTCTGCCGTT 60
TAATTAAAGG GGGGGT 76

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

GTACACCCCC CCCAGGCCG GCCCCCCCCC CCCTTTAATT AAACGGCAGA CAAAAAAAT 60
GTCGCACAAT CTGCG 75

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

GGGGGGGTGT ACATTCAAAT ATGTATCCGC TCATG 35

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

GGGTTACATC GAACTGGATC TC

22

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

CCAGTTCGAT GTAACCCACT CGCGCACCCA ACTGATCCTC AGCATCTTTT ACTTTCACC

59

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

ACTCTAGCTT CCCGGCAACA GTTAATAGAC TGGATGGAGG CGG

43

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

CTGTTGCCGG GAAGCTAGAG TAAG

24

(2) INFORMATION FOR SEQ ID NO: 317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

CCCCCCTTA ATTAAGGGGG GGGGCCGGCC ATTATCAAAA AGGATCTCAA GAAGATCC

58

(2) INFORMATION FOR SEQ ID NO: 318:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

GGGGGGGGCT AGCACGCGCC CTGTAGCGGC GCATTAA

37

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

CCCCCCTGT ACATGAAATT GTAAACGTTA ATATTTTG

38

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

GGGCGATGGC CCACTACGAG AACCATCACC CTAATC

36

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GGGGGGAGAT CTAATAAGAT GATCTTCTTG AG

32

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

GAGTTGGTAG CTCAGAGAAC CTACGAAAAA CCGCCCTGCA AGGCG

45

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

GTAGGTTCTC TGAGCTACCA ACTC

24

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

GTTTCCCCCT GCGGCTCCC TCCTGCGCTC TCCTGTTTCCT GCC

43

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

AGGAGGGAGC CGCCAGGGGG AAAC

24

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

GACATCAGCG CTAGCGGAGT GTATAC

26

- (2) INFORMATION FOR SEQ ID NO: 327:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

GATCTCATAA CTTCGTATAA TGTATGCTAT ACGAAGTTAT TCA

43

- (2) INFORMATION FOR SEQ ID NO: 328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GATCTGAATA ACTTCGTATA GCATACATTA TACGAAGTTA TGAGA

45

- (2) INFORMATION FOR SEQ ID NO: 329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

GGGGGGGAGA TCTGACCAAA ATCCCTTAAC GTGAG

35

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GGTATCTGCG CTCTGCTGTA GCCAGTTACC TTCGG

35

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

CCCCCCCCT AGCCATGTGA GCAAAGGCC AGCAA

35

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

GGGACGTCGG GTGAGGTTCC AAC

23

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

CCATACGGAA CTCGGGTGA GCATTCATC

29

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

CCGGAGTTCC GTATGG

16

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

ACGTTTAAAT CAAAACTGG

19

(2) INFORMATION FOR SEQ ID NO: 336:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

CCAGTTTTGA TTAAACGTA GCCAATATGG ACAACTTCTT CGCCCCCGTT TTCACTATGG
GCAAATATT

60

69

(2) INFORMATION FOR SEQ ID NO: 337:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

GGAAGATCTA GCACCAGGCG TTAAAG

26

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:
GAGGCCGGCC ATCGAATGGC GCAAAAC 27

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:
CGCGTACCGT CCTCATGGGA GAAATAATA C 31

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:
CCATGAGGAC GGTACGCGAC TGGGCGTGGA GCATCTGGTC GCATTGGGTC ACCAGCAAAT 60
CCGCTGTTAG CTGGCCCATT AAG 83

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:
GTCAGCGGCG GGATATAACA TGAGCTGTCC TCGGTATCGT CG

42

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:
GTTATATCCC GCCGCTGACC ACCATCAAAC

30

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(ix) FEATURE:

(A) NAME/KEY: conflict
(B) LOCATION: replace(42..44, "")
(D) OTHER INFORMATION: /note= "in Fig.35b, M41, LAC6: T4T;
but see Fig.35a, M41: LAC6 pos.1055-1119 on
complementary strand, 1076 to 1078: TAT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

CATCAGTGAA TCGGCCAACG CGCGGGGAGA GCGGTTTGC GTATTGGGAG CCAGGGTGGT 60
TTTTC 65

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

GGTTAATTAA CCTCACTGCC CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GCTGCATCAG 60
TGAATCGGCC AAC 73

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

CTAGACTAGT GTTTAAACCG GACCGGGGGG GGGCTTAAGG GGGGGGGGGG 50

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

CTAGCCCCCC CCCCCCTTAA GCCCCCCCCC GGTCCGGTTT AAACACTAGT

50

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

CTAGACTAGT GTTTAAACCG GACCGGGGGG GGGCTTAAGG GGGGGGGGGG

50

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

CCCCCCTTA AGTGGGCTGC AAAACAAAAC GGCCTCCTGT CAGGAAGCCG CTTTATCGG

60

GTAGCCTCAC TGCCCGCTTT CC

82

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:
GTTGTTGTGC CACGCGGTTA GGAATGTAAT TCAGCTCCGC

40

(2) INFORMATION FOR SEQ ID NO: 350:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:
AACCGCGTGG CACAACAAC

19

(2) INFORMATION FOR SEQ ID NO: 351:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:
CTTCGTTCTA CCATCGACAC GACCACGCTG GCACCCAGTT G

41

(2) INFORMATION FOR SEQ ID NO: 352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

GTGTCGATGG TAGAACGAAG

20

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

CCACAGCAAT AGCATCCTGG TCATCCAGCG GATAGTTAAT AATCAGCCCA CTGACACGTT 60
GCGCGAG 67

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

GACCAGGATG CTATTGCTGT GG

22

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

CAGCGCGATT TGCTGGTGGC CCAATGCGAC CAGATGC

37

(2) INFORMATION FOR SEQ ID NO: 356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

CACCAGCAAA TCGCGCTG

18

(2) INFORMATION FOR SEQ ID NO: 357:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

CCCGGACTCG GTAATGGCAC GCATTGCGCC CAGCGCC

37

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

GCCATTACCG AGTCCGGG

18

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

AATCCACCA TCATCACCAT TGACGTCTA

29

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

AGCTTAGACG TCAATGGTGA TGATGGTGG

29

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic gene cassette"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: complement (280..1137)
- (D) OTHER INFORMATION: /product= "bla resistance"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

CGCGTTAACC TCAGGTGACC AAGCCCCTGG CCAAGGTCCC GTACGTTCGA AGATTACCAT 60
 CACGTGGATC CGGTACCAGG CCGGCCATTA TCAAAAAGGA TCTCAAGAAG ATCCTTTGAT 120
 CTTTCTACG GGTCTGACG CTCAGTGGAA CGAAACTCA CGTTAAGGA TTTTGGTCAT 180
 GAGATTATCA AAAAGGATCT TCACCTAGAT CCTTTTAAAT TAAAAATGAA GTTTTAAATC 240
 AATCTAAAGT ATATATGAGT AAACCTGGTC TGACAGTTAC CAATGCTTAA TCAGTGAGGC 300
 ACCTATCTCA GCGATCTGTC TATTTCTGTC ATCCATAGTT GCCTGACTCC CCGTCGTGTA 360
 GATAACTACG ATACGGGAGG GCTTACCATC TGGCCCCAGT GCTGCAATGA TACCGCGAGA 420
 CCCACGCTCA CCGGCTCCAG ATTTATCAGC AATAAACCAG CCAGCCGGAA GGGCCGAGCG 480
 CAGAAGTGGT CCTGCAACTT TATCCGCCTC CATCCAGTCT ATTAAGTGT GCCGGAAGC 540
 TAGAGTAAGT AGTTCGCCAG TTAATAGTTT GCGCAACGTT GTTGCCATTG CTACAGGCAT 600
 CGTGGTGTCA CGCTCGTCGT TTGGTATGGC TTCATTGAGC TCCGGTCCC AACGATCAAG 660
 GCGAGTTACA TGATCCCCCA TGTGTGCAA AAAAGCGGTT AGCTCCTTCG GTCCTCCGAT 720
 CGTTGTCAGA AGTAAGTTGG CCGCAGTGTT ATCACTCATG GTTATGGCAG CACTGCATAA 780
 TTCTCTTACT GTCATGCCAT CCGTAAGATG CTTTCTGTG ACTGGTGAGT ACTCAACCAA 840
 GTCATTCTGA GAATAGTGTA TGCGGCGACC GAGTTGCTCT TGCCCGGCGT CAATACGGGA 900
 TAATACCGCG CCACATAGCA GAACTTTAAA AGTGCTCATC ATTGGAAAAC GTTCTTCGGG 960
 GCGAAACTC TCAAGGATCT TACCGCTGTT GAGATCCAGT TCGATGTAAC CCACTCGTGC 1020
 ACCCAACTGA TCTTCAGCAT CTTTACTTTT CACCAGCGTT TCTGGGTGAG CAAAAACAGG 1080
 AAGGCAAAAT GCCGCAAAA AGGAATAAG GCGACACGG AAATGTTGAA TACTCATACT 1140
 CTCCTTTTTT CAATATTATT GAAGCATTTA TCAGGGTTAT TGTCTCATGA GCGGATACAT 1200
 ATTTGAATGT ACTCGCCGC ACGAGCTGCA GCGCCATTA ATGGCTCGAG CGCGCTTCAG 1260
 CGCTTTGTCT TCCGGATGTA CATGAAATT 1289

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
 1 5 10 15
 Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80
 Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125
 Asp Asn Thr Ala Ala Asn Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
 165 170 175
 Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
 180 185 190
 Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
 195 200 205
 Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
 210 215 220
 Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
 225 230 235 240
 Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
 245 250 255
 Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
 260 265 270
 Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
 275 280 285

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

GCCCTGCAAG CGGAAGAC

18

- (2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

GGCTTTCGAA TGGCCAAAGG

20

- (2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 25..27
- (D) OTHER INFORMATION: /product= "random codon by trinucleotide mutagenesis (ACT/GTT)"

- (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 37..39

(D) OTHER INFORMATION:/product= "random codon by
trinucleotides (TTT,CAT,CTT,ATG,CAG)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:43..45
(D) OTHER INFORMATION:/product= "random codon by
trinucleotides (18 codons, no Pro, no Cys)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:46..48
(D) OTHER INFORMATION:/product= "random codon by
trinucleotides (GAT, GGT, AAT, TCT, TAT)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:49..51
(D) OTHER INFORMATION:/product= "random codon by
trinucleotides (GAT, GGT, AAT, TCT)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:52..54
(D) OTHER INFORMATION:/product= "random codon by
trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:55..57
(D) OTHER INFORMATION:/product= "random codon by
trinucleotides (CCT/TCT)"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION:58..60
(D) OTHER INFORMATION:/product= "random codon by
trinucleotide mutagenesis (19 aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

GCCCTGCAAG CGGAAGACTT TGCGRYTTAT TATTGCHWKC AGNNKDVTDV TNNKYCTNNK 60

ACCTTTGGCC ATTCGAAAGC C 81

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:37..39
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (TTT,CAT,CTT,ATG,CAG)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:43..45
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (18 codons, no Pro, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:46..48
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:49..51
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:52..54
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:55..57
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CCT/TCT)"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION:58..60
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19 aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

GCCCTGCAAG CGGAAGACGT GGGCGTGTAT TATTGCHWKC AGNNKDVTDV TNNKYCTNNK 60

ACCTTTGGCC ATTCGAAAGC C 81

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION:37..39
 (D) OTHER INFORMATION:/product= "random codon by trinucleotides (TTT,CAT,CTT,ATG,CAG)"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION:43..45
 (D) OTHER INFORMATION:/product= "random codon by trinucleotides (18 codons, no Pro, no Cys)"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION:46..48
 (D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT, TAT)"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION:49..51
 (D) OTHER INFORMATION:/product= "random codon by trinucleotides (GAT, GGT, AAT, TCT)"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION:52..54
 (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION:55..57
 (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CCT/TCT)"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION:58..60
 (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19 aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

GCCCTGCAAG CGGAAGACGT GCGGGTGTAT TATTGCHWKC AGNNKDVTDV TNNKYCTNNK 60
 ACCTTTGGCC ATTCGAAAGC C 81

(2) INFORMATION FOR SEQ ID NO: 368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:41..43
 - (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CGT, TGG, TAT)"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:47..61
 - (D) OTHER INFORMATION:/product= "random codons by trinucleotides (18 aa, no Trp, no Cys)"

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:62..64
 - (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

CCTGCAAGCG GAAGACGAAG CGGATTATTA TTGCCAGAGC YRKGACNNKN NKNNKNNKNN 60
 KNNKGGCGGC GGCACGAAGT TAACCGTTCT TGGCCAGGAA TTCGAGCC 108

(2) INFORMATION FOR SEQ ID NO: 369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION:41..43
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CGT, TGG, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION:47..58
- (D) OTHER INFORMATION:/product= "random codons by trinucleotides (18 aa, no Trp, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION:59..61
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

CCTGCAAGCG GAAGACGAAG CGGATTATTA TTGCCAGAGC YRKGACNNKN NKNNKNNKNN 60
KGGCGGCGGC ACGAAGTTAA CCGTTCTTGG CCAGGAATTC GAGCC 105

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "synthetic oligonucleotide library"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION:41..43
- (D) OTHER INFORMATION:/product= "random codon by trinucleotides (CGT, TGG, TAT)"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION:47..55
- (D) OTHER INFORMATION:/product= "random codons by trinucleotides (18 aa, no Trp, no Cys)"

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION:56..58
- (D) OTHER INFORMATION:/product= "random codon by trinucleotide mutagenesis (19aa, no Cys)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

CCTGCAAGCG GAAGACGAAG CGGATTATTA TTGCCAGAGC YRKGACNNKN NKNNKNNKGG 60
CGGCGGCACG AAGTTAACCG TTCTTGCCA GGAATTCGAG CC 102

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "synthetic oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

GGCTCGAATT CCTGGCC

17

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Glu Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala
1 5 10 15
Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu
20 25 30
Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly
35 40 45
Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly
50 55 60
Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln
65 70 75 80
Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr
85 90 95
Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly
100 105 110

Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu
 115 120 125
 Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr
 130 135 140
 Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn
 1 5 10 15
 Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln
 20 25 30
 Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala
 35 40 45
 Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn
 50 55 60
 Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val
 65 70 75 80
 Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu
 85 90 95
 Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala
 100 105 110
 Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe
 115 120 125
 Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val
 130 135 140
 Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 145 150 155